### SEARCH REQUEST FORM

	and reen	nical Information Center
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Requester's Full Name: 10	114 Junize	Examiner #: /65% Date:
Art Unit: /(253 Pho	one Number 30	Examiner # : 7(538 Date:  Serial Number: 09 (444281
Wall Box and Bldg/Room Loca	ation:	Results Format Preferred (circle): PAPER DISK E-MAIL
If more than one search is su	shmittad: mlassst.	*4*
	~~~~~~~~~~~	oritize searches in order of need. ***********************************
- rease provide a detailed statement of	I the search tonic and doca	miles 'C' 11
utility of the invention. Define any to	es, keywords, synonyms, a	acronyms, and registry numbers, and combine with the concept or
known. Please attach a copy of the co	ver sheet, pertinent claims	acronyms, and registry numbers, and combine with the concept or all meaning. Give examples or relevant citations, authors, etc, if
Title of Invention:		
Inventors (please provide full names	s):	
Forlingt Delevity, D.V.		
Earliest Priority Filing Date:		
*For Sequence Searches Only* Please in appropriate serial number.	iclude all pertinent informati	on (parent, child, divisional, or issued patent numbers) along with the
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Match
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1: pir1:*
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protein F18G5.2 [i
ferredoxin-NADP re
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RESULT 2 VGIHHC VGIHHC  22 VGIHHC  E2 91ycoprotein precursor - human coronavirus (strain 22 N;Alternate names: peplomer glycoprotein; S glycoprotein C;Species: human coronavirus A;Note: host homo sapiens (man) C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text, C;Accession: A34766; S05460 R;Raabe, T.; Schelle-Prinz, B.; Siddell, S.G. T. Gen virol 71 1065-1073 1000	Similarity 88.9%; Pred. No. 0.014; 8; Conservative 1; Mismatches 0 www. 11	nne (NCBIP licted <si <pro="" licted=""> rimental (Arg) (am DB 1;</si>	PIDN:CAA4 ; Tang, tridecape	RESULT 1  JC1222  indolicidin precursor - bovine N; Alternate names: antimicrobial peptide C; Species: Bos primigenius taurus (cattle) C; Date: 10 -Sep - 1999 #sequence_revision 10 -Sep - 1999 #te: C; Accession: JC1222; A42387; S25664 R; del Sal, G.; Storici, P.; Schneider, C.; Romeo, D.; Biochem. Biophys. Res. Commun. 187, 467-472, 1992 A; Title: CDNA cloning of the neutrophil bactericidal paragraphy. Reference number: JC1222; MUID:92392368; PMID:152033	ALIGNMENTS	30 44 51.2 967 2 C70831 31 44 51.2 968 2 F70746 32 44 51.2 968 2 T00322 33 44 51.2 1154 1 VGIHJB 34 44 51.2 1162 1 VGIHJB 35 44 51.2 1162 2 S07421 36 44 51.2 1162 2 S14939 37 44 51.2 1162 2 S14940 38 43.5 50.6 276 2 AH0244 43 50.0 192 2 A59189 40 43 50.0 192 2 H86543 41 43 50.0 192 2 H86543 42 43 50.0 192 2 D702081 43 43 50.0 236 2 J02086 44 43 50.0 236 2 A83506 44 43 50.0 278 2 T46458
229E) sin; spike glycoprotein xt_change 16-Jun-2000		:83840)  G> <pre> <mat> ide in mature form from following Length 144;</mat></pre>	7755.1; PID:g463 Y.Q.; Smith, W.; Cullor, J.S. ptide amide from neutrophils. 821	<pre>#text_change 10-Sep-1999  D.; Zanetti, M.  al peptide indolicidin.  20337</pre>		probable mmpL4 pro hypothetical prote E2 glycoprotein pr probable esterase ATP-binding casset light harvesting p hypothetical prote conserved hypothet arylesterase (EC 3) probable cobalamin hypothetical prote

J.

Gen. Virol. 71, 1065-1073, 1990

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C;Keywords: glycoprotein: transmembrane protein
F;1-15/Domain: signal sequence #status predicted <SIG>
F;1-15/Pomain: signal sequence #status predicted <MAT>
F;16-1173/Product: E2 glycoprotein #status predicted <TMN>
F;1116-1138/Domain: transmembrane #status predicted <TMN>
F;23,62,98,147,171,176,220,243,326,333,440,464,518,538,542,568,581,587,663,671,930,1015.
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A; Molecule type: mRNA
A; Residues: 1-1173 < RAA>
A; Cross-references: EMBL: X16816; NID: 958926;
A; Cross-references: strain 229E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Nucleotide sequence of the human coronavirus HCV A;Reference number: A34038; MUID:89366667; PMID:2701946 A;Accession: S05460
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Nucleic Acids Res. 17, 6387, 1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein DKFZp434C192.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 23-Jul-1999
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 23-Jul-1999
C;Accession: T12505
R;Ansorge, W.; Wirkner, U.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, June 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: 217527
A; Reference number: 717527
A; Statum: 712505
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A; Residues: 1159-1173 <RA2>
                                                                                         C; Date: 17. (2) 29295
C; Accession: T29295
R; Johnson, D.; Stellyes, L.
submitted to the EMBL Data Library, November 1995
submitted to the EMBL Data Library, November 1995
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                                                                                                                                                                                hypothetical protein C50F7.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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A;Experimental source: adult testis;
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A; Residues: 1-299 <ANS>
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                                                            A; Reference number: Z20601
A; Accession: T29295
                 A; Molecule
                                 A; Status: preliminary; translated
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type: DNA
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5; Conserve
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62.5%;
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85.7%;
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16;
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7.9;
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A;Cross-references: EMBL:U41557; PIDN:AAA83303.1; CESP:C50F7.8 C;Genetics: A;Gene: CESP:C50F7.8
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Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating A;Reference number: A75000; MUID:99069613; PMID:9851916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein F18G5.2 [imported] - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 10-May-2001 #sequence_revision 10-May-2001 C;Accession: E89605
                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Bos primigenius taurus (cattle)
C;Date: 14-Jul-1994 #sequence_revision 18-oct-1996 #text_change 03-Jun-2002
C;Accession: JT0751; JT0079; JS0390; S03558; PS0003; A29604; S52100
R;Takata, Y; Sagara, Y; Kono, A.; Sekimizu, K.; Horiuchi, T.
Biol. Pharm. Bull. 16, 1200-1206, 1993
A;Title: Gene structure of bovine adrenodoxin reductase.
A;Reference number: JT0751; MUID:94177140; PMID:8130767
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A; Residues: 1-467 <STO>
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A; Accession: E89605
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                                                                              A; Title: Cloning and sequence analysis of adrenodoxin reductase A; Reference number: JT0079; MUID:88198050; PMID:3448086
A; Accession: JT0079
A; MOID:88198050; PMID:3448086
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-204, 211-498 < SAG>
A; Cross-references: GB:D00211; NID:g217433; PIDN:BAA00150.1; PIDA; Note: the deduced sequence is partially confirmed by amino aci
                                                                                                                                                                                                                                                                                                                  A;Residues: 1-498 <TAK>
A;Cross-references: GB:D83475; NID:g1199916; PIDN:BAA11921.1; PID:g4521308
A;Experimental source: adrenal cortex
              submitted to DDBJ, September 1989 A; Reference number: JS0390
                                                                                                                                                                                                                                           A;Note: the authors translated the codon GTC for residue 205 R;Sagara, Y.; Takata, Y.; Miyata, T.; Hara, T.; Horiuchi, T. J. Blochem. 102, 1333-1336, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: JT075
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83.3%;
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Pred. No.
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Pred. No. 4.2;
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22;
205-210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 467;
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                                                                                             acid
                                                                                                                   PID: g217434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bovine
                                                                                                                                                                                                                                    cDNA from
                                                                                                                                                                                                                                                                                                           Gly
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revision,

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residues

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A; Molecule type: protein
A; Residues: 33-41,'S',43-62;260-283,'TM';496-498 <HAM>
A; Residues: 33-41,'S',43-62;260-283,'TM';496-498 <HAM>
A; Note: a cyanogen bromide peptide binds to adrenoferredoxin
R; Nonaka, Y.; Murakami, H.; Yabusaki, Y.; Kuramitsu, S.; Kagamiyama, H.; Yamano, T.; Oka Biochem. Biophys. Res. Commun. 145, 1239-1247, 1987
A;Title: Molecular cloning and sequence analysis of full-length cDNA for mRNA of adrenod A; Reference number: A29604; MUID:87270696; PMID:3038094
A; Molecular cloning and sequence analysis of full-length cDNA for mRNA of adrenod A; Reference number: A29604; MUID:87270696; PMID:3038094
A; Molecular cloning and sequence analysis of full-length cDNA for mRNA of adrenod A; Reference number: A29604; MUID:87270696; PMID:3038094
                                                                                                                                                         hypothetical protein SCE36.09 - Streptomyces coelicolor C; Species: Streptomyces coelicolor C; Species: Streptomyces coelicolor C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999 C; Accession: T36208 R; Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajano
                                                                                                                                                                                                                                                                                                                               RESULT 7
T36208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R.HanuKOglu, I.; Gutfinger, T.
Bur. J. Biochem. 180, 479-484, 1989
A;Title: cDNA sequence of adrenodoxin reductase. Identification of NADP-binding sites
A;Reference number: S03558; MUID:89170752; PMID:2924777
A;Accession: S03558
A; Status: p
A; Molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-76, 'K', 78-80, 'VWLALTTPRSRMLL', 95-123, 'RVYRLT', 129-204, 211-273, 'R', 275-322,
A; Cross-references: GB:M17029; NID:g162628; PIDN:AAA30362.1; PID:g162629
A; Experimental source: adrenal cortex
R; Warburton, R.J.; Seybert, D.W.
Biochim. Biophys. Acta 1246, 39-46, 1995
A; Title: Structural and functional characterization of bovine adrenodoxin reductase by l
A; Reference number: $52100; MUID:95110846; PMID:7811729
                                                                                                                         R;Oliver, K.; Harris, D.; Bentley, submitted to the EMBL Data Library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: protein
A;Residues: 'X',34-41,'X',43-48,'X',50-51;304-306,'X',308-309,'X',311-326 <WAR>
C;Comment: Ferredoxin NADP+ reductase is localized in the matrix of adrenal cortex mitocerredoxin-NADP+ reductase, adrenodoxin and two forms of cytochrome P-450.
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A;Title: Adrenoferredoxin-binding peptide of NADPH-adrenoferredoxin
A;Reference number: PS0003; MUID:88184054; PMID:3355838
A;Accession: PS0003
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A;Residues: 155-204,211-498 <HAN>
A;Cross-references: EMBL:X13736; NID:g65;
                                                              A;Reference number: Z21601
A;Accession: T36208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R; Hamamoto, I.; Kurokohchi,
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                           preliminary;
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5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         11
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                                                                                                                         Data Library,
                        translated
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83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                               from GB/EMBL/DDBJ
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                                                                                                                         S.D.;
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A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SCF75 ^^
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A;Authors: Parry, C.; Quail, M.; Rutherford, K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Date: 09-Nov-2001 #sequence_revision C;Accession: AH0755 R;Parkhill, J.; Dougan, G.; James, K.D. th, T.; Connerton, P.; Cronin, A.; Davi
                                                                                                                                                                                                               R:Park, H.J.; Kreutzer, R.; Reiser, C.O.A.; Sprinzl, M. Eur. J. Biochem. 205, 875-879, 1992 A;Title: Molecular cloning and nucleotide sequence of the A;Reference number: S23449; MUID:92249331; PMID:1577004 A;Accession: S23449
                                                                                                                                                                                                                                                                                         NADH oxidase (H202-forming) (EC 1.6.-.) - Thermus aquaticus C;Species: Thermus aquaticus C;Decies: 2-Jan-1993 #sequence_revision 22-Jan-1993 #text_change C;Accession: S23449; S24556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:AL513382; PIDN:CAD05747.1; PID:g16503239; GSPDB:GN00176 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     conserved hypothetical protein STY2208 [imported] - Salmonel C; Species: Salmonella enterica subsp. enterica serovar Typhi A; Note: this species has also been called Salmonella typhi
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AH0755
                                                                                                                                                    A;Cross-references: EMBL:X60110
A;Accession: S24556
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A; Residues: 1-248 < PAR>
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A; Residues: 1-265 < PAR>
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                                                            F; 1-248/Product:
                                                                           C; Keywords: NAD;
                                                                                            A;Gene: nox
                                                                                                                       A; Molecule type: protein A; Residues: 1-32 < PAR1>
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 Matches
                 Query Match
Best Local
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5; Conser
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                                                                           oxidoreductase
                                                           NADH oxidase (H2O2-forming) #status experimental
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              54.7%;
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80.0%;
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31.6%;
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Pred. No.
              Score 47;
Pred. No.
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Pred. No. 6.
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Davis, P.; Davies, R.
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17;
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Salmonella
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Gaps
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R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Hamlin, N.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Ho Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complet A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: G70715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status; preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Molecule type: DNA A;Rosidues: 1-253 <COL> A;Cross-references: GB:Z79700; GB:AL123456; NID:g3261628; PIDN:CAB02005.1; PID:g1524217 A;Experimental source: strain H37Rv C;Genetics: A;Gene: Rv0945 A;Gene: Rv0945 C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology F;8-190/Domain: short-chain alcohol dehydrogenase homology <SADH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C;Accession: B83161
                                                                                                                                                                                                                                                                                                                                      A; Gene: PA3883
C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:AE004805; GB:AE004091; A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Complete genome see
A;Reference number: A82950;
A;Accession: B83161
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R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.;
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probable moeY protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 2
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    #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
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70.0%;
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Pred. No.
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                                                    A; Experimental source:
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R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Natture 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: B70741
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-715 <COL> A;Cooss-references: GB:Z75555; GB:AL123456; NID:g3261608; PIDN:CAA99988.1; PID:e25035 A;Experimental source: strain H37Rv C;Genetics:
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A; Introns: 281/2;
A; Note: T22P22.90
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A; Residues: 1-1411 <BEV>
A; Cross-references: EMBL: AL163814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Accession: T48529
R;Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, submitted to the Protein Sequence Database, April 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein T22P22.90 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
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A; Accession: T48529
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                                                                                    A; Reference number: Z25286
A; Accession: T51071
A; Status: preliminary
                                                                                                                                                                 R;Schulte, U.; Aign, V.; submitted to the Protein
                                                                                                                                                                                                                C; Accession: T51071
                                                                                                                                                                                                                                    related to trfA protein [imported] - Neurospora crassa N;Alternate names: protein B2A19.50 C;Species: Neurospora crassa C;Species: Neurospora crassa C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000
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A;Cross-references: EMBL:AL390092; GSPDB:GN00116; NCSP:B2A19.50
A;Experimental source: BAC clone B2A19; strain OR74A
                                            A; Molecule type: DNA
A; Residues: 1-728 <SCH>
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Local Similarity 63.6%;
nes 7; Conservation
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                                                                                                                                                                 Hoheisel, J.; Brandt, P.; Fartmann, Sequence Database, July 2000
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Pred. No. 1.1e+02;
Pred. No. 1.1e+02;
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anthranilate synthase (EC 4.1.3.27) component I [validated] - Pseudomonas syringae pv. st. Alternate names: anthranilate synthase alpha chain C:Species: Pseudomonas syringae pv. savastanoi C:Date: 27-Nov-1991 #sequence_revision 27-Nov-1991 #text_change 17-Mar-2000 C:Accession: A39128 R: Silva, O.; Kosuge, T. R: Silva, O.; Kosuge, T. J. Bacteriol. 173, 463-471, 1991 A:Title: Molecular characterization and expression analysis of the anthranilate synthase A:Reference number: A39128; MUID:91100331; PMID:1987141 A:Title: Molecular characterization and expression: A39128 A:Accession: A39128; MUID:91100331; PMID:1987141
                                                                                                                                                                                                                                                                         A;Description: EC 4.1.3.27 [validated, MUID:91100331]
A;Note: expression of trpE seems to be independent of the concentration of tryptophan in C;Superfamily: anthranilate synthase component I C;Keywords: carbon-carbon lyase; oxo-acid-lyase; tryptophan biosynthesis
                                                                                                                                                                                                                                                                                                                                                                           A;Gene: trpE
C;Complex: heterotetramer; two component I chains, two component II chains
C;Function: <ANT>
A;Description: EC 4.1.3.27 [validated, MUID:90130325]
A;Pathway: tryptophan biosynthesis
A;Pathway: tryptophan biosynthesis
A;Note: first step
C;Function: <COM1>
Search completed: January 15, 2003, 18:04:27 Job time: 17 secs
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A; Introns: 26/1; 119/2
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A; Residues: 1-505 < DAC>
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Local Similarity 58.3%;
nes 7; Conservative
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28.0%;
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Pred. No. 67;
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Result
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Maximum Match 100%
Listing first 45 summaries
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MEDLINE=90264837; PubMed=2345367;

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Raabe T., Schelle-Prinz B., Siddell S.G.;

"Nucleotide sequence of the gene encoding the spike glycoprotein numan coronavirus HCV 229E.";

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TISSUE-Adrenal cortex;
MEDLIND-89170752; PubMed-2924777;
Hanukoglu I., Gutfinger T.;
"cDNA sequence of adrenodoxin reductase.
binding sites in oxidoreductases.";
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"Cloning and sequence analysis of adrenodoxin reductase
bovine adrenal cortex.";
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MEDLINE-87270696; PubMed=3038094;
Nonaka Y., Murakami H., Yabusaki Y.,
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                                                                                                                                                                       Molecular cloning and sequence analysis of full-length of adrenodoxin oxidoreductase from bovine adrenal cortex Biochem. Biophys. Res. Commun. 145:1239-1247(1987).
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"Adrenodoxin reductase-adrenodoxin complex structure suggests e 
transfer path in steroid biosynthesis.";
J. Biol. Chem. 276:2786-2789(2001).
-!- FUNCTION: SERVES AS THE FIRST ELECTRON TRANSFER PROTEIN IN.
MITOCHONDRIAL P450 SYSTEMS. INCLUDING CHOLESTEROL SIDE CHAIL 
CLEAVAGE IN ALL STEROIDOGENIC TISSUES, STEROID 11-BETA 
HYDROXYLATION IN THE ADRENAL CORTEX, 25-OH-VITAMIN D3-24 
HYDROXYLATION IN THE KIDNEY, AND STEROL C-27 HYDROXYLATION
                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as modified and this statement is not removed. U entities requires a license agreement (See htt or send an email to license@isb-sib.ch).
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MEDLINE=20455764; PubMed=10998235;
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3L; D83475; BAA11921.1;
JB; D83472; BAA11921.1;
JL; D83473; BAA11921.1;
JL; D83474; BAA11921.1;
JL; D83474; BAA30362.1;
D00211; BAA00350.1;
L; D00211; BAA00350.1;
JC; D00211; BAA00350.1;
L; X13736; CAA32002.1;
Z13736; CAA32002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIVER.
CATALYTIC ACTIVITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Mitochondrial matrix.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; A SHORT FORM (SHOWN LONG FORM; ARE PRODUCED BY ALTERNATIVE SPLICING. THE REPRESENTS 10-20% OF ALL ADRENODOXIN REDUCTASE MRNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               European Bioinformatics Institute.
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een the Swiss Institute of Bioinformatics and the EN
European Bioinformatics Institute. There are no resti
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                                                                      laboratory strains.";
Submitted (APR-2001) to
-!- SIMILARITY: BELONGS
                                                                                                                                                                                                                      "Deciphering the biology of Mycobacterium tuberculosis from complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Putative oxidoreductase Rv0945 (EC 1.-..)
                                                                                                                               Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula
                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D
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         SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no restr
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RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Ollver S., Geborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Rutter S., Seeger K., Whitehead S., Barrell B.G.;
TDeciphering the biology of Mycobacterium tuberculosis from the
Complete genome sequence ";
L. Nature 393:537-544(1998).
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Hypothetical protein; Oxidoreductase; Complete ACT_SITE 159 BY SIMILABIRE SEQUENCE 755.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
Hypothetical protein Rv1355c.
Rv1355c OR MT1398 OR MTCY02B10.19C.
                                                                                                                                                                                                                               Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White (Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzbe Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mik
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01-OCT-1996
                                                                                                                                                                                                                                                                             STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                  Submitted
                                                                                                                                                                                "Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains.";
                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Actinobacteria; Actinobacteria (class); Act:
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Z79700; CAB02005.1; -.
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5; Conserv
                                                                                                                                                                (APR-2001) to the EMBL/GenBank/DDBJ databases.
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100.0%;
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Pred. No.
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8.1;
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Best Local
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Pfam; PF00899; ThiF; 1.

Hypothetical protein; Complete proteome.

Hypothetical protein; Complete 455495248A56041C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P21689;
01-MAY-1991
01-MAY-1991
15-JUN-2002
                                                                                                              EMBL; M55911; AAA26016.1; -.
PIR; A39128; A39128.
HSSP; Q06128; 1QDL.
InterPro; IPR000256; Anth_synth1.
InterPro; IPR000350; Chorlsmate_bind.
Pfam; PF00425; Chorlsmate_bind; 1.
                                                                                                                                                                                                       entities
or send a
                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                pyruvate + L-glutamate.
-!- PATHWAY: Tryptophan biosynthesis; first step.
-!- SUBUNIT: TETRAMER OF TWO COMPONENTS I AND TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                               dda Costa e Silva O., Kosuge T.;
"Molecular characterization and
anthranilate synthase gene of ps
savastanoi.";
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TIGR; MT1398;
                                                                                                                                                                                                                                use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                        J. Bacteriol. 173:463-471(1991).
-!- CATALYTIC ACTIVITY: Chorismate + L-glutamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE=91100331; PubMed=1987141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas syringae (pv. Bacteria; Proteobacteria;
                                                  Tryptophan
SEQUENCE
                                                             TIGRFAMS; TIGR00564; trpE_most; 1. Tryptophan biosynthesis; Lyase.
                                                                                       PRINTS; PR00095; ANTSNTHASEI.
ProDom; PD000779; Chorismate_bind;
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                                                                                                                                                                                                                                                                                                                      USING AMMONIA RATHER THAN GLUTAMINE, WHEREAS COMPONENT II GLUTAMINE AMIDOTRANSFERASE ACTIVITY. SIMILARITY: BELONGS TO THE ANTHRANILATE SYNTHASE COMPONENT
                                                                                                                                                                                                                                                                                                                                                          MISCELLANEOUS: COMPONENT I CATALYZES
                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY).
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6; Conserv
                                                                                                                                                                                                     s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
Similarity 7; Conserv
                                                  biosynthesis; 1 505 AA; 56084
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. 41, Last anno
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66.7%;
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             28.0%;
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Pred. No.
          Pred. No.
                         Score 45.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas
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4.1.3.27).
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                       Length 505;
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RA Gentles S., Goble A., Hamlin N., Harris D., Hadalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neil S., Pearson D., Ouail M.A., Rabbinowitsch E.,
RA Ra Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Ratherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Woodward J., Volckaert G., Aert R., Wansh S.V., Warren T., Whitehead S.,
RA Wolfens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Galilardin C., Tallada V.A., Garzon A., Thode G.,
RA Lucas M., Rochet M., Galilardin C., Tallada V.A., Garzon A., Thode G.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RI Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RI Shakure 415:871-880(2002).
CC ("MDAB)
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Q09677;
01-NOV-1995
                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content endified and this statement is not removed. Usage by an entities requires a license agreement.
                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21848401; PubMed=11859360; Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Syouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Syouros K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SCHPO
                                                                                                                                                                                                                  EMBL; Z49811; CAA89955.1; -.
                                                                                                                                                                                                                                                  entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                              SEQUENCE
                                                                                                                                                             Hypothetical
                                                                                                                                                                        InterPro; IPR003680; NADHdh_2.
Pfam; PF02525; NADHdh_2; 1.
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63
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8; Conser
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(Rel. 32,
(Rel. 41,
                                                                                                                                            196 AA;
                                                                    Conservative
                                                                                                                                                             protein
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Ascomycota; Schizosaccharomycetes;
etales; Schizosaccharomycetaceae;
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FUT3_HUMAN STANDARD; PRT; 361 AA. P21217; Q99448; Q99449; O1-MAY-1991 (Rel. 18, Created) O1-MAY-1991 (Rel. 18, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Molecular cloning of the rat adipocyte hormone-sensitive inhibited cyclic nucleotide phosphodiesterase.";
J. Biol. Chem. 268:18573-18579(1993).
-i- FUNCTION: MAY PLAY A ROLE IN FAT METABOLISM.
-i- CATALYTIC ACTIVITY: Nucleoside 3',5'-cyclic phosphate.
-i- CATALYTIC ACTIVITY: Nucleoside 3',5'-cyclic phosphate.
-i- ENZYME REGULATION: INHIBITED BY CGMP.
-i- SUBCELLULAR LOCATION: Membrane-bound (Potential).
-i- TISSUE SPECIFICITY: ABUNDANT IN ADIPOSE TISSUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ethe European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by are entities requires a license agreement (See http://www.isb-
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15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
cGMP-inhibited 3',5'-cyclic phosphodiesterase B (EC 3.1.4.17) (Cyclic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00233; PDEase; SMART; SM00471; HDc: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Taira M., Hockman S.C., Calvo J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Sprague-Dawley; TISSUE=Adipose tissue; MEDLINE=93366761; PubMed=8395509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GMP inhibited phosphodiesterase B) (CGI-PDE B) (CGIPDE1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CN3B_RAT
                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Z22867; CAA80489.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Manganiello V.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003607;
InterPro; IPR002073;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
                                                                                                                                                                                    164 WQWWSWLR 171
                                                                                                                                                                                                                                                                 Local Similarity hes 5; Conserv
                                                                                                                                                                                                                        4 WPWWPWRR 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cGMP; Membrane
                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HDC;
                                                                                                                                                                                                                                                                                                                                                AA;
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102
179
1021
1021
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                                                                                                                                                                                                                                                                                    52.3%;
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POLY-ASP.
POLY-GLU.
                                                                                                                                                                                                                                                                                    Score 45; DB
Pred. No. 58;
                                                                                                                                                                                                                                                                                                                                                                   POLY-GLU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POLY-PRO
                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                C9B5078C7D3ADD6D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               It is produced through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Taira M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ā
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                                                                                                                                                                                                                                                                                                         Length 1108;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a collaboration
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Kukowska-Latallo J.F., Larsen R.D., Nair R.P., I "A cloned human cDNA determines expression of a embryonic antigen and the Lewis blood group alpha(1,3/1,4) fucosyltransferase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Galactoside 3(4)-L-fucosyltransferase (EC 2.4.1.65) (Blood alpha-4-fucosyltransferase) (Lewis FT) (Fucosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=95378269; PubMed=7650030;
Cameron H.S., Szczepaniak D., Weston W.;
"Expression of human chromosome 19p alpha(1,3)-fucosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=91032981;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rahim I., Schmidt L.R., Wahl D., Drayson E., Maslan Stranahan P.L., Pettijohn D.E.; "Isolation and expression of human alpha (1,3/1,4) fucosyltransferase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genes in normal tissues. Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARIANTS LE(-) ARG-20;
MEDLINE=94059082; PubMe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Elmgren A., Rydberg L., Larson "Genotypic heterogeneity among
                                                                                                                                                                                              Mollicone R., Reguigne I., Kelly R.J., Fletcher A., Watt J., Chatfileld S., Raiz A., Cameron H.S., Weston B.W., Lowe J.B., "Molecular basis for Lewis alpha(1,3/1,4)-fucosyltransferase deficiency (FUT3) found in Lewis negative Indonesian pedigree
                                                                                                                                                                                                                                                                                                                                                                                                VARIANTS LE(-) ARG-20 MEDLINE=94033579; Pub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a single amino acid substitution individuals.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Narimatsu H.;
"Alpha (1,3/1,4)fucosyltransferase (FucT-III) gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nishihara S., Yazawa S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochem. Biophys. Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=94059067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (FEB-1999) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Squamous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      isoforms
                                                  "Molecular genetic system.";
                                                                                                                                                                                                                                                                                                                          mucosa of Lewis-positive and Blood 82:2915-2919(1993).
                                                                                                                                                                                                                                                                    VARIANTS LE(-) ARG-20 AND LYS-356.
MEDLINE=94342259; PubMed=8063716;
                                                                                                                                                                                                                                                                                                                                                            "Analysis of Lewis fucosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                 Koda Y., Kimura H.,
 VARIANTS
                                                                                                                        MEDLINE=95050753;
                                                                                                                                                                                 Biol.
                                   Biol.
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                                                                                                                                             LE(-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biophys. Res.
LE(-)
                                     Chem.
                                                                                        senO T., Narimatsu H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Human)
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                                                                                                                                           LYS-356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      270:20112-20122(1995)
 ARG-20;
                                     269:29271-29278(1994).
                                                                                                                                                                               269:20987-20994(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cell carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=1977660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=8240322;
                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=8219240;
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                                                                                                                        PubMed=7961897;
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Primates;
                                                                     analysis
                                                                                                                                                                                                                                                                                                                                                                                   Mekada E.;
                                                                                                                                                                                                                                                                                                                                                                                                                     AND SER-170
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Commun.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SER-170 AND
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   ARG-68; MET-105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wahl D., Drayson E., Maslanik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Iwasaki H.,
                                                                     I.;
of the human
                                                                                                         Iwasaki H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                             -negative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lewis negative individuals."; 196:515-520(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           196:624-631(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALA-336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lewis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        splicing, polyadenylation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nakazato
                                                                                                                                                                                                                                                                                                                                             genes from the human e individuals.";
   AND LYS-356
                                                                                                             Yazawa
                                                                           Lewis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            histo-blood
                                                                                                                                                                                                    Indonesian pedigrees.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lowe J.B.;
mouse stage-specific
                                                                         histo-blood
                                                                                                             s.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kudo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             is
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                                                                                                             Akamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Σ.
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3) (FUCT-
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                                                                           group
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(POTENTIAL).

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N-LINKED (GLCNAC.

L -> R (IN LE(-)).

/FTId-VAR\_003426.

W -> R (IN LE(-)). LUMENAL, CATALYTIC

TRANSMEM DOMAIN

VARIANT VARIANT Signal-anchor;

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EMBL; X53578; CAA37641.1; -.
EMBL; U27328; AAC50187.1; -.
EMBL; U27326; AAC50186.1; -.
EMBL; U27327; AAC50186.1; -.
EMBL; D89324; BAA13941.1; -.
EMBL; D89325; BAA13941.1; -.
EMBL; AR131913; AAD33514.1; -.
EMBL; AR131913; AAD33514.1; -.
EMBL; A36669; A3669; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'FUT3' gene enables molecular group system.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Elmgren A., Boerjeson C., Svensson L., Rydberg L., Larson "DNA sequencing and screening for point mutations in the l'TUT3' gene enables molecular genotyping of the human Lewi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alpha'1,3/1,4'-fucosyltransferase, Fu
J. Biol. Chem. 272:21994-21998(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Significance of individual point mutations, T2() munan Levis 'FUT3' gene for expression of Lewis alpha'1,3/1,4'-fucosyltransferase, Fuc-TIII.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Elmgren A., Mollicone R.,
Harrington J., Larson G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=96243526; PubMed=8801770;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97413801;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       between the Swiss Institute of Bioinformat
the European Bioinformatics Institute. The
use by non-profit institutions as long
modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genew;
                                                                                                                                                                                                                                                                                                                                                                                               Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Toit E.D., Kimura H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PATHWAY: Glycosylation.
SURCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUI
FORM IN TRANS CISTERNAE OF GOLGI.
TISSUE SPECIFICITY: HIGHLY EXPRESSED IN STOMACH, COLON, SMALI
INTESTINE, LUNG AND KIDNEY AND TO A LESSER EXTENT IN SALIVAR:
GLAND, BLADDER, UTERUS AND LIVER.
GLAND, BLADDER, UTERUS ON THE CORRESPONDING 1,4-GALACTOSYL
DERIVATIVE, FORMING 1,3-L-FUCOSYL LINKS.
SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sang. 70:97-103(1996)
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CATALYTIC ACTIVITY: GDP-L-fucose + 1,3-beta-D-galactosyl-N-acetyl-D-glucosaminyl-R = GDP + 1,3-beta-D-galactosyl-(alpha-acetyl-D-glucosaminyl-R = GDP + 1,3-beta-D-galactosyl-(alpha-acetyl-D-galactosyl-D-galactosyl-D-galactosyl-D-galactosyl-(alpha-acetyl-D-galactosyl-D-galactosyl-D-galactosyl-D-galactosyl-D-ga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INVOLVED IN THE EXPRESSION OF VIM-2, LEWIS A, LEWIS B, STALYL LEWIS X AND LEWIS X/SSEA-1 ANTIGENS. MAY BE INVOLVED IN BLOOD GROUP LEWIS DETERMINATION; LEWIS-POSITIVE (LE(+)) INDIVIDUALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1,4-L-fucosyl)-N-acetyl-D-glucosaminyl-R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            111100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HGNC:4014; FUT3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR001503; GT_10
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                                                                                                                                                                                                                                                         Glycosyltransferase; Glycoprotein; Transmembrane; r; Golgi stack; Polymorphism; Blood group antigen.

1 15 CYTOPLASMIC (POTENTIAL).
16 34 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ARG-68 AND MET-105.
101; PubMed=9268337;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Glyco_transf_10; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             South Africa.";
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Best Local S
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            This SWI
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the Euro
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Costache M., Apoil P.-A., Cailleau A., Elmgren A., Larson G.,
Henry S., Blancher A., Tordachescu D., Oriol R., Mollicone R.;
"Evolution of fucosyltransferase genes in vertebrates.";
"Evolution of fucosyltransferase genes in vertebrates.";
J. Biol. Chem. 272:29721-29728 (1997).
-I- FUNCTION: MAY CATALYZE ALPHA-1,3 AND ALPHA-1,4 GLYCOSIDIC LINKAGES INVOLVED IN THE EXPRESSION OF SIALYL LEWIS X AND LEWIS X/SSEA-1 ANTIGENS. IT MAY BE INVOLVED IN BLOOD GROUP LEWIS DETERMINATION
                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Galactoside 3(4)-L-fucosyltransferase (EC 2.4.1.65) (Blood alpha-4-fucosyltransferase) (Lewis FT) (Fucosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUT3_PANTR
019058;
                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                    alpha-4-fucosyltransferase) (Lewis III) (Alpha-3/4-fucosyltransferase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota;
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                                                                                               PATHWAY: Glycosylation.
SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND FORM IN TRANS CISTERNAE OF GOLGI (BY SIMILARITY).
POLYMORPHISM: THERE ARE TWO ALLELES (A AND B). ALLELE A HAS AR POLYMORPHISM: THERE ARE TWO ALLELES (A AND MET-304.

162 AND VAL-304. ALLELE B HAS GLY-162 AND MET-304.
                                                            MISCELLANEOUS: ALSO ACTS ON THE CORRESPONDING 1 DERIVATIVE, FORMING 1,3-L-FUCOSYL LINKS.
SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE
                                                                                                                                                                       CATALYTIC ACTIVITY: GDP-L-fucose + 1,3-beta-D-galactosyl-N-acetyl-D-glucosaminyl-R = GDP + 1,3-beta-D-galactosyl-(alpha-1,4-L-fucosyl)-N-acetyl-D-glucosaminyl-R.
            SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                     (BY SIMILARITY)
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zoa; Chordata;
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V -> M (IN LE(-)).

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D -> A (IN LE(-)).

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T -> M (IN LE(-)).

/FTId=VAR_003427.
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Pred. No.
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G -> S (IN LE(-); COMPLETELY INACTIVE).
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/FTId=VAR_003428
G -> R (IN LE(-)
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           ne EMBL outstation restrictions on it
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3) (FUCT-
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01-OCT-1996
16-OCT-2001
                                                                                                                                                                                                                                                                                                            Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
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CARBOHYD
VARIANT
                                                       "Whole genome comparison of Mycobacterium tube laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ-i-SUBCELLULAR LOCATION: Integral membrane pro-i-SIMILARITY: BELONGS TO THE MMPL FAMILY.
                                                                                                                                                   STRAIN-CDC 1551 / Oshkosh; Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg Kolonay J.F., Nelson W.C., Umayam L.A., Khouri H., Gill J., Mikula Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula
                                                                                                                                                                                                                                                             Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis complete genome sequence."; Nature 393:537-544(1998).
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              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - \frac{1}{2}
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Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
                                                                                                                                          Bishai W.;
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PQWPWRR
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372 AA;
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(Rel. 34, Last sequence update)
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162
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14 CYTOPLASMIC (POTENTIAL)
34 SIGNAL-ANCHOR (TYPE-II
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85.7%;
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15-JUN-2002 (Rel. 36, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
Hypothetical protein C23C11
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Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.; "The genome sequence of Schizosaccharomyces pombe."; Nature 415:871-880(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
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RESULT 13
MML4_MYCTU
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Matches
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A Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Har Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Har Gordon S.V., Elglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., A Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holro A., Davies R., Devlin K., Krogh A., McLean J., Muzhy L., Hornsby T., Jagels K., Krogh A., McLean J., Muzhy D., Muzhy T., Jagels K., Krogh A., Rajandream M.A., Rogers J., A Rutter S., Seeger K., Skelton S., Squares S., Squares R., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Rutter S., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."
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053735;
30-MAY-2000 (Rel.
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16-OCT-2001 (Rel.
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (S or send an email to license@isb-sib.ch).
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TRANSMEM
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                                                                                                                                                                                                          Nature
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Putative membrane protein mmpL4.
MMPL4 OR RV0450C OR MT0466 OR MTV037.14C
                                                                                                                                                                                                                                                                                                                                                                                                                                           Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium tuberculosis.
                                                                                                                     Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula
                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN-CDC 1551 /
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Actinobacteria;
                                                                  laboratory strains.";
Submitted (APR-2001) to
                                                                                                                                                                STRAIN=CDC 1551 / Oshkosh; Fleischmann R.D., Alland D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      183 WSWSPSTWPWRQ 194
This SWISS-PROT entry is copyright. between the Swiss Institute of Bio:
                                        -!- SUBCELLULAR LOCATION:
                                                                                                           Bishai W.;
                                                                                               "Whole
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
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135
163
221
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Corynebacterineae; Mycobacteriaceae; Mycobacterium
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75 POTENTIAL.
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63 POTENTIAL.
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                                        N: Integral membrane protein TO THE MMPL FAMILY.
                                                                    the EMBL/GenBank/DDBJ
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                                                                                               Mycobacterium tuberculosis clinical
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Pred. No. 40;
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  jht. It is produced through a collaboration
Bioinformatics and the EMBL outstation ^
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               update)
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                                                                                   MEDLINE-98295987; PubMed-9634230;
GCole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544(1998).
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                                                                                                                                                                                                                                                                                                                01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
Putative membrane protein mmpL2.
MMPL2 OR RV0507 OR MT0528 OR MTCY20G9
                                                                                                                                                                                                                                                                                                                                                                                                   MYCTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
EMBL;
TIGR;
        SEQUENCE FROM N.A.

STRAIN-CDC 1551 / Oshkosh;

Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,

Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,

Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,

Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg

Belcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula
                                                                                Nature
[2]
                                                                                                                                                                                                                                                                                                                                                                            MML2_MYCTU
Q11171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit modified and this si entities requires a
                                                                                                                                                                                                                                   STRAIN-H37Rv;
                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis
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AE006949;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   id and this statement is not remo
s requires a license agreement (
an email to license@isb-sib.ch)
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242 26
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AAK44689.1;
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75.0%;
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Pred. No.
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Best Local S
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Lamers W., Clevers H.;
"High expression of the
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TISSUE=Embryo;
MEDLINE=98201614; PubMed=9524265;
                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                        SOX-13 protein.
SOX13 OR SOX-13
                                                                                                                                                                                                                                                                                                                         30-MAY-2000
15-JUN-2002
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Q04891;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR004707;
InterPro; IPR004869;
Pfam; PF03176; MMPL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no resuse by non-profit institutions as long as its content
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBCELLULAR LOCATION: Integral membrane -!- SIMILARITY: BELONGS TO THE MMPL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    laboratory strains."; Submitted (APR-2001) to the EMBL/GenBank/DDBJ
                                                                                    embryonic
                                                                                                                                                                     TISSUE=Embryo;
                                                                                                                                                                                       SEQUENCE
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                                                                    Nucleic
                                                                                                                                                     MEDLINE-98083175; PubMed-9421502,
                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                           01-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical
                                   SEQUENCE
                                                                                                                                                                                                                       NCBI_TaxID=10090;
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Rodentia;
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Search completed: January 15, 2003, 18:03:28 Job time: 13 secs
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"Cloning and characterization of mouse mSox13 cDNA.";
Gene 208:201-206(1998).
[3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE-93181275; PubMed-8441686;
MIDITUME-93181275; PubMed-8441686;
MIDITUME-93181275; PubMed-8441686;
MIDITUME-93181275; PubMed-8441686;
MIDITUME MEMBERS OF THE SEQUENCE 5'-AACAAT-3'.
-!- FUNCTION: BINDS TO THE SEQUENCE 5'-AACAAT-3'.
-!- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
-!- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
                                                                                                                                                                                          VARSPLIC
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EMBL; AB006329; BAA25786.1; --
EMBL; 218962; CAA79487.1; --
PIR; S30241; S30241.
HSSP; Q05066; 1HRY.
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MGD; MGI:98361; Sox13.

InterPro; IPR000910; HMG_12_box.

Pfam; PF00505; HMG_box; 1.

SMART; SM00398; HMG; 1.
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                                                               686 WPWWTKLAEGFSPW 699
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ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; MAY BE PRODUCED BY ALTERNATIVE SPLICING.

PRODUCED BY ALTERNATIVE SPLICING.

TISSUE SPECIFICITY: IN THE EMBRYO, HIGH LEVELS OF EXPRESSION ARE FOUND IN THE ARTERIAL WALLS AT 13.5 DAYS POST COITUM (DPC). LOW ENTRY ARE FOUND IN THE INNER EAR AT 13.5 DPC AND IN SOME CELLS IN THE THYMUS AT 16.5 DPC EXPRESSED IN THE TRACHEAL EPITHELIUM BELOW THE TYPOCAL CORD AND IN THE HAIR FOLLICLES AT 18 DPC.

SIMILARITY: CONTAINS 1 HMG BOX.
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195
984 AA;
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610
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159 195 GLN-RICH.
397 465 HMG BOX.
495 519 PGCSPKLHHPVSRPSLVARGGLA
                                                                                                                                Conservative
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984 MI
35 P
42 AT
195 Q
196 WW;
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42.9%;
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MISSING (IN ISOFORM 2).
P -> L (IN REF. 2).
AT -> TN (IN REF. 2).
Q -> QQ (IN REF. 2).
Q; 7F5506EDADEB98C5 CRC64;
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HMG BOX.
PGCSPKLHHPVSRPSLVARGGLWLL -> QGARQSYTIP
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1 ILRWPWWPWRRK 1
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sp_mammal:*
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sp_archeap:*
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Q9CZA1
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O99dna1 tt virus. o
O990ma human coron
O900ma human
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Q9duc9
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9 tt virus. o
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Q9s751 oryza sativ	р	pse					Q8s697 oryza sativ	∍	tt vi	Q94ef3 oryza sativ	Q8tww9 methanopyru	Q9r6j3 agrobacteri	arabidopsi			oryza sati	Q8v7e2 tt virus. o	$\Box$	_		streptom	Q91d04 tt virus. o		Q988w4 rhizobium l	caenc	Omo	homo	Q9dt80 tt virus. o

# ALIGNMENTS

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DT Q1DD Q1
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01-MAR-2001
01-MAR-2001
01-JUN-2002
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Virology 277:368-378(2000).
EMBL; ABO(1959; BAB19313.1;
Interpro; IPRO01563; Serine_carbpept.
Interpro; IPRO04219; TTVirus_Unk.
Pfam; PF02956; TT_ORF1; 1
PROSITE: PS00131; CARBOXYPEPT_SER_SER; UNKNOWN_1.
SEQUENCE 723 AA; 85393 MW; 232D003098766344 CRC64;
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TT virus.
Viruses; ssDNA viruses;
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Okamoto H., Nishizawa T., Tawara A., Peng Y., Takahashi M.,
Kishimoto J., Tanaka T., Miyakawa Y., Mayumi M.;
"Species-specific TT viruses in humans and nonhuman primates and their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN=MF-TTV9;
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PWWPWRR 8
                                                                                                                           Similarity 7; Conserv
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2 (TrEMBLrel.
                                                                                                                           Conservative
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                                                                                                                        66.3%; Score 57; DB
100.0%; Pred. No. 8.1
Live 0; Mismatches
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                                                                                                                                                      DB 12; Length 723;
8.8;
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Best Local Similarity
Matches 6; Conserv
Best Local Similarity Matches 5; Conserv
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01-OCT-2000
01-OCT-2000
01-JUN-2002
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                                                                                                                                      "Viral and cellular changes in a human cell line persistently infected with human coronavirus HCOV-229E.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF344186; AAK32188.1; ...
InterPro; IPR002551; Corona_S1.
InterPro; IPR002552; Corona_S2.
Pfam; PF01600; Corona_S1; 1.
Pfam; PF01601; Corona_S2; 1.
SEQUENCE 1173 AA; 128669 MW; ABC6E0A75E8BD8A4 CRC64;
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01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AB028669; BAA94878.1; -
Interpo; IPR004219; TTVirus_Unk.
Pfam; PF02956; TT_ORF1; 1.
SEQUENCE 746 AA; 88561 MW; E0
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Ukita M., Okamoto H., Nishizawa T., Tawara A., Takahashi N
Iizuka H., Miyakawa Y., Mayumi M.;
"The entire nucleotide sequences of two distinct TT virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JUN-1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Viruses; ssRNA positive-strand viruses, Coronaviridae; Coronavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q990M4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-TJN02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=11137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Spike glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bonavia A., Holmes K.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=229E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human coronavirus (strain 229E)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            isolates."
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   Conservative
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54.5%;
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62.5%;
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Last annotation update)
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Pred. No.
                                     Pred. No. 42;
                                                                      Score 53; DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                      Length 1173;
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Best Local Similarity
Matches 5; Conserv
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Q990M2;
01-JUN-2001 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
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Q990M3;
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 19,
                                                                                  "Viral and cellular changes in a human cell line persistently infected with human coronavirus HCOV-229E.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AR344188; AAK32190.1; ...
InterPro; IPR002551; Corona_S1.
InterPro; IPR002551; Corona_S2.
Pfam; PF01600; Corona_S1; 1.
Pfam; PF01601; Corona_S2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human coronavirus (strain 229E).
Viruses; ssRNA positive-strand viruses,
Coronaviridae; Coronavirus.
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"Viral and cellular changes in a human cell line persistently

"Viral and cellular changes in a human cell line persistently

with human coronavirus HCoV-299E.";

Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AF344187; AAK32189.1;

InterPro; IPR002551; Corona_S1.

InterPro; IPR002552; Corona_S2.
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                                                                                                                                                                                                                                                      Human coronavirus (strain 229E).
Viruses; ssRNA positive-strand viruses,
Coronaviridae; Coronavirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=229E;
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                                                                                                                                                                                                    STRAIN=229E;
                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                          NCBI_TaxID=11137;
                                                                                                                                                                                        Bonavia A., Holmes K.V.;
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                          Score 53; DB Pred. No. 42; 2; Mismatches
                           2;
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                                                                                           STRAIN-BKL/0; STRAIN-BKL/0; MEDILINE-9338943; PubMed-8397280; Bridgen A., Duarte M., Tobler K., Laude H., Ackermann M.; Bridgen A., Duarte M., Tobler K., Laude H., Ackermann M.; "Sequence determination of the nucleocapsid protein gene of the porcine epidemic diarrhoea virus confirms that this virus is a porcine related to human coronavirus 229E and porcine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q84712;
Q84712;
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Q990M1;
  STRAIN-BR1/87;
                    SEQUENCE FROM N.A
                                                             coronavirus related to human coronavirus transmissible gastroenteritis virus."; J. Gen. Virol. 74:1795-1804(1993).
                                                                                                                                                                                                                      STRAIN-BR1/87
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN-BR1/87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 porcine epidemic diarrhea virus Viruses; ssRNA positive-strand of Coronaviridae; Coronavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Spike
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Pfam; PF01601; Corona_S2; 1.
SEQUENCE 1173 AA; 128760 MW;
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                                                                                                                                                                                                                                                                                                                                                   Duarte M.,
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                      SEQUENCE FROM STRAIN=CV777;
                                                                                                                  MEDLINE=98455678; PubMed=9782358; Bridgen A., Kocherhans R., Tobler K., Carvajal
                                                                                                                                                             SEQUENCE FROM N.A. STRAIN=CV777;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=93389433; PubMed=8397280;
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  Kocherhans
                                                                                                                                                                                                                                   "PEDV leader sequence
                                                                                                                                                                                                                                                       Pobler K., Ackermann M.;
                                                                                                                                                                                                                                                                          MEDLINE=96112302; PubMed=8830538;
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Duarte M., Tobler K., Bridgen A.,
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Duarte M., Tobler K., Bridgen A.,
                                                                                                  Further analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                       Laude H.;
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the genome of porcine
440:781-786(1998).
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380:541-542(1995).
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01-JUN-2002
01-JUN-2002
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

KANG T.-J., Lim Y.-Y., Jang Y.-S., Kwon T.-H.,

"Spike Protein gene of Korea Porcine Epidemic

Submitted (APR-2002) to the EMBL/GenBank/DDBJ

EMBL; AF500215; AAM19716.1; -.

SEQUENCE 1386 AA; 151853 MW; 11F98BCB2AA05
       Puyesky M., Benhamou N., Ponce Noyola P., Bauw G., Van Montagu M., Herrera Estrella A., Horwitz B.A.; "Developmental regulation of comply a gene encoding Conidlospore surface protein of Trichoderma."; Fungal Genet. Biol. 27:88-99(1999).
EMBL; AJ133651; CAB40845.1; ".
                                                                                                                                                                                                                                                                      1324
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                                                                     SEQUENCE FROM N.A.
STRAIN=ATCC 32173;
MEDLINE=9934881; PubMed=10413618;
                                                                                                              Hypocreales; mit
NCBI_TaxID=5544;
                                                                                                                         Eukaryota; Fungi; Ascomycota;
Hypocreales; mitosporic Hypocr
                                                                                                                                                                  Conidiospore
                                                                                                                                                                            01-NOV-1999
01-JUN-2002
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Coronaviridae; Coronavirus.
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InterPro; IPR002552; Corona_S2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (FEB-2001) to the EMBL; AF353511; AAK38656.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           coronavirus.
                                                                                                                                               Trichoderma
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AJ133651;
P01180; 1N
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62.5%;
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Hypocreales; Trichoderma.
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ne Epidemic 1
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c Diarrhea Virus.
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Best Local Similarity
Matches 5; Conser
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Complete proteome.
Complete 298 AA;
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Q8ZU59;
01-MAR-2002
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InterPro; IPR001673; S_mold_repeat.
ProDom; PD006869; S_mold_repeat; 2.
PROSITE; PS01346; CLAUDIN; UNKNOWN_1.
PROSITE; PS01346; CLAUDIN; UNKNOWN_1.
                                                                                          Ayportal Ayportal (Human).

Homo sapiens (Human).

Homo sapiens (Human).

Homo sapiens (Human).

Horia; Metazoa; Chordata; Metazoa; Primates;
              ....usuye w., wirkner U., Mewes H.W., Gassenhube Submitted (JUN-1999) to the EMBL/GenBank/DDBJ EMBL; AL096753; CAB46428.2; -..
                                                                                                                                    Q9Y4N1 PRELIMINARY; PRT; 299 (9Y4N1); Q9Y4N1; C1940N1; C1-2000 (TrEMBLrel. 12, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence 01-MAY-2000 (TrEMBLrel. 13, Last annotatine through the total 34.0 kDa protein (Fragment). DKFZP434C192.
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                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
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Archaea; Crenarchaeota;
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01-JUN-2002
Hypothetical
NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Miller J.H.;
                                                        TISSUE=TESTIS;
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Pfam; PF00809; Pterin_bind; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                       aerophilum."
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                                                                    SEQUENCE FROM N.A.
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Pred. No.
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Pred. No.
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                                                                                                     Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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01-JUN-2001 (Tr
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2810031J10Rik;
2810031J10RIK.
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01-MAY-1997
01-JUN-2002
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             Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito
                                                                                        SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-EMBRYO;
MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
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Submitted (DEC-1996) to
EMBL; Z83214; CAB05671.
HSSP; P00800; 1HYT.
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Bacteria; Firmicutes; Bacillus/Clostridium
Thermoactinomycetaceae; Thermoactinomyces.
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Pfam; PF01447; Peptidase_M4; 1.
Pfam; PF02868; Peptidase_M4_C; 1.
SEQUENCE 504 AA; 56653 MW; 5A7;
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01-JUN-2001 (TrEMBLrel. 17, La
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Hypothetical 36.7 kDa protein
OSJNBA0058E19.18.
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Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=4530;
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Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA
Nature 409:885-690(2001).
EMBL; AK012846; BAB28508.1; -
MGD; MGI:1919917; 2810031J10Rik.
InterPro; IPR003309; Treg_SCAN.
Pfam; PF0203; SCAN; 1.
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., Santos L., Zutavern T., l
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Q9ITV2	Q9ITX8	Q9CK19	Q9W1W7	Q9Y0E8	070458	088821	Q99AQ7	Q9IU37	Q9BXY6	Q9HC40	094516	Q90644	Q9YRR9	P97692	Q8VI99	Q63779	Q63289	Q9XAE4	Q9ADM1	Q94EF3	Q99AQ3	P72844	Q9LQN0	Q66765	Q9X8C2	Q91CY5	Q9A7E1	QBTVMB
Q9itv2	Q9itx8	Q9ck19	Q9w1w7	Q9y0e8	070458	088821	Q99a	Q9iu37	Q9bxy6	Q9hc40	094516	090644	Q9yrr9	p97692	Q8vi99	Q63779	Q63289	Q9xae4	Q9adm1	Q94ef3	Q99aq3	P72844	Q91q	Q66765	Q9x8c2	Q91cy5	Q9a7e1	Q8tvm8
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STRAIN-ATCC 32173;
MEDLINE-99343881; PubMed=10413618;
MEDLINE-99343881; PubMed=10413618;
MEDLINE-99343881; PubMed=10413618;
Menchamou N., Ponce Noyola P., Bauw G., Ziven Montagu M., Herrera Estrella A., Horwitz B.A.;
"Developmental regulation of cmpl. a gene encoding a reconstitution of Tichoderma.";
Conidiospore surface protein of Tichoderma.";
Fungal Genet. Biol. 27:88-99(1999).
EMBL; AJ133651; CAB40845.1; -.
HSSP; P01180; 1NPO.
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1185 RWQWWSWPRRGRG------CWQWWSW 1204
                                                                                                                                                                                                                                                                                                                     InterPro; IPR001832; Claudin.
InterPro; IPR001673; S_mold_repeat.
ProDom; PD006869; S_mold_repeat; 2.
PROSITE; PS01346; CLAUDIN; UNKNOWN_1.
SEQUENCE 1245 AA; 135824 MW; 3249C749AFAOCDF8 CRC64;
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NCBI_TaxID=5544;
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9; Conserv
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29.0%;
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Pred. No. 2.
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RESULT 2
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AC Q9JH
AC Q9JH
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RP SEQUE
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01-MAR-2001
01-JUN-2002
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Q9DUC4;
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EMBL; AB028669; BA94878.1; .
InterPro; IPR004219; TTVirus_Unk.
Pfam; PF02956; TT_ORF1; 1.
SEQUENCE 746 AA; 88561 MW; E01
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01-ОСТ-2000
                                                                                                                                                   MEDLINE-20534983; PubMed=11080484; Okamoto H., Nishizawa T., Tawara A., Peng Y., Tal Kishimoto J., Tahaka T., Mayakawa Y., Mayumi M.; "Species-specific TT viruses in humans and nonhum phylogenetic relatedness."; Virology 277:368-378(2000).
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01-JUN-2002
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Similarity 33.3%;
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Liu Z.H., Lu
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SEQUENCE 49 AA: 7776.--
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Pfam; PF0;
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"TT virus mRAs detected in
individual.",
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EMBL; AF371370; AAK54733.1; -.
InterPro; IPR004219; TTvirus_Unk.
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Sai T., Sugai Y.;
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RESULT Q9Z8B7

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01-MAR-2001
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EMBL; AE0001625; AAD18570.1; -.
EMBL; AE002194; AAF38182.1; -.
EMBL; AP002546; BAA98634.1; -.
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Q9Z8B7;
Q9Z8B7;
01-MAY-1999
01-MAY-1999
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CT277 SIMILAI
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TT virus.
  MEDLINE=20568739; PubMed=11118348; Okamoto H., Nishizawa T., Tawara A Sai T., Sugai Y.; "TT virus mRNAs detected in the her-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg White O., Hickey E.K., Peterson J., Utterback T., Berry Linher K., Weidman J., Kohouri H., Craven B., Bowman C., Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Eisen J., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                              Q9DT81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MADLINE=99206606; PubMed=10192388; Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Olinger L., Grimwood J., Davis R.W., Stephens R.S.; "Comparative genomes of Chlamydia pneumoniae and C. tranat. Genet. 21:385-389(1999).
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CPN0426 OR CPJ0426 OR CP0327.
Chlamydia pneumoniae (Chlamydophila pneumoniae).
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydop
                                                                                         STRAIN-TYM9;
                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                   Viruses;
                                                                                                                                                                                                                                                                                                                  Q9DT81;
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16,
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Last annotation updat
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  the bone marrow
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                                          Takahashi M.,
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K., Bass
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Salzberg S.L.,
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01-DEC-2001
01-JUN-2002
           D'Ambrosio E., Waitzkin S.D., Witney F.R.,
"Structure of the highly repeated, long int
or LIRn) of the rat.";
Mol. Cell. Biol. 6:411-424(1986).
EMBL; M13100; AAA66046.1; -.
InterPro: IPR000566; Lipocln_cytFABP.
PROSITE; PS00213; LIPOCALIN; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          multiple tissues from infected humans Virology 288:558-368(2001).
EMBL; AB060592; BAB69900 l; -.
InterPro; IPR004219; TTvirus_Unk.
                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Hypothetical 43.7 kDa protein.
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                                                                                                                                                                    MEDLINE=87064324; PubMed=3023845;
                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                             Q63778;
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                                                                                                                                                                                          TISSUE=LIVER;
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Yoshikawa A.;
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Q8V7E2;
Q1-MAR-2002
Q1-MAR-2002
Q1-JUN-2002
QRF1 (Fragme)
TT virus.
                                           SEQUENCE FROM N.A.

STRAIN-AN19 / DSM 6324 / JCM 9639;

STRAIN-AN19 / DSM 6324 / JCM 9639;

MEDLINE-21927647; PubMed=11930014;

Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N., Shekarbinina O.V., Shakhova V.V., Belova G.I., Aravind L., Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter I Malykh A.G., Koonin E.V., Kozyavkin S.A.;

Malykh A.G., Koonin E.V., Kozyavkin S.A.;

"The complete genome of hyperthermophile Methanopyrus kandles and monophyly of archaeal methanogens.";

Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).

EMBL; AE010396; AAM02288.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       viremic infants.";
Arch. Virol. 147:21-41(2002).
EMBL; AB064615; BAB79374.1; -.
EMBL; AB064615, Trvirus_Unk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=21844401; PubMed=11855633;
MEDLINE=21844401; PubMed=11855633;
                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
NAD-dependent protein deacetylase, SIR2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Analysis of the complete genomes of thirteen TT virus variants classifiable into the fourth and fifth genetic groups, isolated
                                                                                                                                                                                                                                                                                                                                                                                                          NAD-dependent
SIR2 OR MK1075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Okamoto H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Viruses; ssDNA viruses;
NCBI_TaxID=68887;
    Complete SEQUENCE
                                                                                                                                                                                                                                                                                                                                         Methanopyrus
                                                                                                                                                                                                                                                                                                                                                       Methanopyrus kandleri.
Archaea; Euryarchaeota;
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ER 92 92
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13; Conserv
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250 AA;
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Pred. No.
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      B051994FE5B24E05 CRC64;
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Best Local
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Q8V711;
01-MAR-2002
01-MAR-2002
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Q1-DEC-2001 (TrEMBLrel. 19,

Q1-DEC-2001 (TrEMBLrel. 19,

Q1-DEC-2001 (TrEMBLrel. 19,

Q1-DEC-2001 (TremBLrel. 19,
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Lycopersicon esculentum (Tomato).
Eukaryota; Viridiplantae; Streptc
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Physical, Plantarum 0:0-0(2001).
EMBL, AY205037; AAK08984.1; -.
SEQUENCE 284 AA; 23434 MW; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Uthappa M.,
                                                                             viremic infants.";
Arch. Virol. 147:21-41(2002).
EMBL; AB064598; BAB79322.1; -.
InterPro; IPR004219; TTVirus_Unk.
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A STRAIN=CT43F;
                                                                                                                                                                                                                                                                                                                                                                                                                     Viruses; ssDNA viruses; NCBI_TaxID=68887;
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                                                                                                                                                           "Analysis of the complete classifiable into the four
                                                                                                                                                                                                                          MEDLINE-21844401; PubMed-11855633;
Peng Y.H., Nishizawa T., Takahashi
                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                           Submitted (JUL-2001)
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"Thappa M., Muchhal U.S., Baldwin J.C., Raghothama K.G.;

"LeGRP1: A new member of glycine-rich proteins from tomato".
                                                                                                                                                                                                     Okamoto H.;
                                                                                                                                                                                                                                                                STRAIN=CT43F;
                                                                                                                                                                                                                                                                                                                                                Okamoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TT virus.
                                       SEQUENCE
                                                             Pfam;
                                                                                                                                                                                                                      Peng Y.H., Nishizawa
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                                          PF02956;
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AA; 8697
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Pred. No.
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                                            F60E188BC0104A68 CRC64;
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Best Local Similarity 32.3%; Matches 10; Conservative

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Okamoto H., Nishizawa T., Tawara A., Peng
Kishimoto J., Tanaka T., Miyakawa Y., May
"Species-specific TT viruses in humans an
"hylogenetic relatedness.";
Virology 277:368-378(2000)
EMBL; AB041957; BAB19308.1;
Interpro; IPR004219; TTVirus_Unk.
Pfam; PF02956; TT_ORF1; 1.
SEQUENCE 735 AA; 86132 MW; 9ED818D6BE
                                                                                                                                                                                                                                   Q98414
Q98414;
Q1-FEB-1997
Q1-FEB-1997
Q1-DEC-2001
                                                                                                                                                                       Ovine lentivirus.
Viruses; Retroid viruses;
NCBI_TaxID=11663;
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01-FEB-1997 (TrEMBLrel. 02,
01-DEC-2001 (TrEMBLrel. 19,
Envelope glycoprotein.
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STRAIN-85/34; Carlson J.O., DeMartini J.C., Mwaengo D.M.; "Envelope glycoprotein nucleotide sequence
                                                                                                MEDLINE=95135990; PubMed=7834396; Woodward T.M., Carlson J.O., de la Demartini J.C.;
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                                     SEQUENCE FROM N.A.
                                                            "Biological and genetic changes in ovine lentivirus strains passage in isogeneic twin lambs.";
L. Acquir. Immune Defic. Syndr. Hum. Retrovirol. 8:124-133(1
                                                                                                                                     STRAIN-85/34;
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Best Local
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                                                                                                                                                                               characterization of North American ovine lentiviruses.";
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U64439; AAB08725.1; -.
                                                                                                                                    Transmembrane.
SEQUENCE 985 AA;
                                                                                                                                                          InterPro; IPR000328; Pfam; PF00517; GP41;
                                           163 ILKRVYKQDWPWNTYHWPLWQMENMRQWMKENEREYKGRTNKTKEDIDDLLAGKIRGRFC 222
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                                                                  ILKK-----WPW----WP----
VPYPFALLKCTKWCWYP
                      ---PIMILK--KWPWWP 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Search time 11 Seconds (without alignments) 139.511 Million cell updates/sec
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Compugen
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   P35954
P12723
P112723
P112650
P11650
P12651
P021465
Q014405
Q014405
Q0144624
P23422
                                                                                                                                                                                                            P96862
P57990
P15423
Q9y5q5
Q9x319
P48628
Q9x8c5
P03379
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P35581
                                                                                                                                                                                                                                                                                                                                                                                             P31627
P16899
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Q53902
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Q45633
                                                                                                                                                                                                                                                                                                                                                                                                                           P50655 anas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
                                                                                                                                                                                                            5 homo sapien
9 mus musculu
9 glycine max
5 aythya amer
5 human adeno
5 escherichia
9 visna lenti
 2 avian infec

3 avian infec

3 avian infec

1 avian infec

5 avian infec

5 avian infec

5 bacteriopha

9 neisseria m

6 neisseria m

6 neisseria m

7 brassica na

2 arabidopsis

2 visna lenti
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bacillus st
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apis mellif
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lenti
P33046;
01-OCT-1993 (Rel. 2
01-OCT-1993 (Rel. 2
01-NOV-1997 (Rel. 2
                                                                                                                                                                                                                                                                                                                                                                                             J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                         neutrophils.";
J. Biol. Chem.
                                             SIGNAL
                                                            Antibiotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cullor J.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INDC_BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                       "Indolicidin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Bovine).
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# ALIGNMENTS

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PIR; JC1222; JC1222.
PIR; A42387; A42387.
InterPro; IPR001894; C
Pfam; PF00666; Catheli
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PROPEP
PEPTIDE
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                       InterPro; IPR001894; Cathelicidin.
Pfam; PF00666; Cathelicidins; 1.
Probom; PD001838; Cathelicidin, 1.
PROSITE; PS00944; CATHELICIDINS_1;
PROSITE; PS00947; CATHELICIDINS_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Ch
Mammalia; Eutheria; Ce
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Neutrophils;
MEDLINE=92165771; PubMed=1537821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X67340; CAA47755.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Biol. Chem. 267:4292-4295(1992).

-i- FUNCTION: POTENT MICROBICIDAL ACTIVITY, ACTIVE AGAINST STAPHYLOCOCCUS AUREUS AND ESCHERICHIA COLI.

-i- TISSUE SPECIFICITY: LARGE GRANULES OF NEUTROPHILS.

-i- PTM: ELASTASE MIGHT BE RESPONSIBLE FOR ITS MATURATION.

-i- SIMILARITY: BELONGS TO THE CATHELICIDIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Selsted M.E., Novotny M.J., Morris W.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indolicidin precursor.
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131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  novel bactericidal
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     29
130
143
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                                                                                                                                                                                                           Signal.
                                                       INDOLICIDIN
                                                                                                                                                                     POTENTIAL.
     PYRROLIDONE CARBOXYLIC ACID (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A
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                                                                                                                                                                                     RESULT 3
POLG_EMCV
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Query Match
Best Local (
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Best Local
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Q45633;
30-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAY 2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 35.7 kDa protein in mala 3'region
Bacillus stearothermophilus.
Bacteria; Firmicutes; Bacillales; Geobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                    p03304;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Genome polyprotein [Contains: Coat proteins VPI TO VP4;
P2A TO P2C, P3A; Genome-linked protein VPG; Picornain 3C
(EC 3.4.22.28) (Protease 3C) (P3C); RNA-directed RNA pol
(EC 2.7.7.48))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Molecular cloning of a maltose transport gene
stearothermophilus and its expression in Escher
Mol. Gen. Genet. 243:343-352(194).
-i- SIMILARITY: BELONGS TO THE UPF0097 FAMILY.
                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein. SEQUENCE 314 AA; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=ATCC 7953;
MEDLINE=94247374; PubMed=8190087;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN=ATCC 7953;
                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR004175; 2_5_1 Pfam; PF02834; 2_5_ligase;
                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; L13418; AAA71981.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Liong E.C., Ferenci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=1422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126
              Cardiovirus
                         Encephalomyocarditis virus. Viruses: ssRNA positive-str
                                                                                                                                                                        POLG_EMCV
                                                                                                                                                                                                                                             222
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nes 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 EAEPIMILKKWPWWPWRR 36
                                                                                                                                                                                                                                                                        N
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                                                                                                                                                                                                                                             LKQWQWEQAKARWEAERDADGARREPGETWDFLLDKPSWWERLIGRWRR
                                                                                                                                                                                                                                                                       LKKWPWWPWRRKHEAEPEA----EP----IMILKKWPWWP-----WRR 36
                                                                                                                                                                                                                                                                                                    l Similarity
17; Conserv
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107
143
144 AA;
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                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                            positive-strand viruses,
                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32.4%;
55.6%;
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                                                                                                                                                                                                                                                                                                                                                          35735 MW;
                                                                                                                                                                                                                                                                                                                  25.7%;
                                                                                                                                                                                                                                                                                                                                                                                   2_5_ligase.
yase; 2.
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BY SIMILARITY.
BY SIMILARITY.
ANIDATION (G-144 PROVIDE AMIDE GROUP).
FEBBLCBBE55C09911 CRC64;
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                                                                                                                                                                                                                                                                                                    Score 62; DB 1; Length 314; Pred. No. 0.99; 5; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                           PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      port gene from Bacillus
in Escherichia coli K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.0049;
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                             no
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                             DNA
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                               stage;
                                                                     RNA polymerase
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                                Picornaviridae
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RESULT 4
MMLA_STRCO
ID MMLA_S'
AC Q53902
DT 30-MAY
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                                                                                     밁
                                                                                                                                                 Query Match
Best Local S
                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The nucleotide and deduced amino acid sequences of the encephalomyocarditis viral polyprotein coding region."; nucleic Acids Res. 12:2969-2985(1984).

-i- FUNCTION: P3C POLYPEPTIDE IS A PROTEASE THAT CLEAVES AT CERTAIN PURCEION: P3C POLYPEPTIDE IS A PROTEASE THAT CLEAVES AT CERTAIN Q/G SITES IN THE POLYPROTEIN. IT MAY BE A CYSTEINE PROTEASE.

-I- CAPALYTIC ACTIVITY: Selective cleavage of Gin-1-Gly bond in the
                                                                                                                                                                                   ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                         PROPEP
CHAIN
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=84169586; PubMed=6324136; Palmenberg A.C., Kirby E.M., Janda M.R., Drake
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=12104;
                                                                                                                                                                                                                                   CHAIN
                                                                                                                                                                                                                                              CHAIN
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00073; rhv; 3. Pfam; PF00680; RNA_dep_RNA_pol; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000605; RNA_helicase.
InterPro; IPR001205; RNA_pol_P3D.
InterPro; IPR001676; Rhv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Potratz K.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                      LIPID
                                                                                                                                                                                                                                                                                                                                                                             Polyprotein; Coat protein; Core protein; Transferase; RNA-directed RNA polymerase; Hydrolase; Thiol protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X00463; CAA25152.1;
                                                                                                                                                                                                                                                                      CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00910;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEROPS; C03.009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A03906;
                                                                                     967
                                                                                                             6 PWWPWRRKHEAEPEAEPI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       poliovirus polyprotein. In other picornavirus reactions Glu me
substituted for Gln, and Ser or Thr for Gly.
CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE I SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    {RNA}(N).
SUBUNIT: THE VIRUS CAPSID IS EACH OF WHICH IS COMPOSED OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VP3, AND VP4.
                                                                                     PWNPWKNTYQAVLRAEPCRVTMDIYYKRVRPFRLPLVQKEWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P12296;
                                                                                                                                     | Similarity
                                                                                                                                                                                                                                   623
911
1057
1193
1518
1606
1626
1831
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                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Collett M.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2MEV.
                                                                                                                                                                                                                                                                                                                                                                                                     RNA_helicase;
                                                                                                                                                                                     ΑA;
                                                                                                                                                                                                                                                                                                                                                                  polymerase;
67
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391
622
910
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1192
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1625
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2290
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                                                                                                                                                                                       W.
                                                                                                                                                                                                                                                                    CORE PROTEIN P2A CORE PROTEIN P2B CORE PROTEIN P2C CORE PROTEIN P3A.
                                                                                                                                       6
                                                                                                                                       Score 59.5; I
Pred. No. 14;
6; Mismatches
                                                                                                                                                                                                                                                                                             CORE
CORE
                                                                                                                                                                                                                                   GENOME-LINKED PROTEIN VPG (H). PICORNAIN 3C (P22). RNA-DIRECTED RNA POLYMERASE P3D
                                                                                                                                                                                                 PROTEASE (POTENTIAL).
PROTEASE (POTENTIAL).
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PROTEIN VP2 (BETA)
PROTEIN VP3 (GAMMA
                                                                                                                                                 No. 14;
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(GAMMA).
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OF PROTEINS V
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MMLA\_STRCO Q53902; 30-MAY-2000

(Rel.

39, Created)

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Fernandez-Moreno M.A., Caballero J.L., Hopwood D.A., Malpartida F.;
"The act cluster contains regulatory and antiblotic export genes,
direct targets for translational control by the blda trNA gene of
Streptomyces.";
                                                                                                             TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                          Hypothetical TRANSMEM 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kleser T., Larke L., Murphy L., Oliver K., O'Neil S., Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S., Squares S., Taylor K., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K., Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
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coelicolor A4(2).";
Nature 417:141-147(2002).
-i- SUBCELLULAR LOCATION: Integral membrane protein
-i- SIMILARITY: BELONGS TO THE MMPL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                 EMBL; AL593842; CAC44197.1; -.
InterPro; IPR004707; ActII.
InterPro; IPR000731; HMGCR/patch_5TM.
InterPro; IPR0007869; MMPL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=A3(2) / M145;
MEDLINE=21996410; PubMed=12000953;
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Streptomyces coelic
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NCBI_TaxID=1902;
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ENV_CAEVG

ID ENV_CAEVG

RAC P31627;

AC P31627;

DT 01-JUL-1993 (Rel. 26, Created)

DT 16-OCT-2001 (Rel. 40, Last seque)

DT 16-OCT-2001 (Rel. 40, Last annot)

Env polyprotein precursor (Coat be protein; Transmembrane protein].

GN ENV.

OS Caprine arthritis encephalitis voc viruses; Retroid viruses; Retrovoc viruses; Retroid viruses; Retrovoc NCBI_TaxID-11662;

RN (1)

RP SEQUENCE FROM N.A., AND SEQUENCE RX MEDLINE-92015464; PubMed-1656067

RA KNOWles D.P. Jr., Cheevers W.P., RA Harwood W.G., Stem T.A.;
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J. Mol. Evol.
-!- FUNCTION:
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TRANSMEM
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01-OCT-1996 (Rel.
15-JUN-2002 (Rel.
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Hydrogen ion transport; CF(0); Mitochondrion;
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MEDLINE=94047124; Pu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: Membrane-bound.
-!- SIMILARITY: BELONGS TO THE ATPASE PROTEIN 8 FAMILY.
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9; Conser
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Bioinformatics Institute.
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(Rel. 41, Last annotation
protein 8 (EC 3.6.3.14)
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PubMed=8230253;
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rsor (Coat polyprotein)
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Retroviridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Structure and genetic variability of envelope glycoproteins of two antigenic variants of caprine arthritis-encephalitis lentivirus."; Virol. 65:5744-5750(1991).
      ENV_OMVVS
P16899;
01-AUG-1990
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0517; GP41;
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC
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EMBL; M31646; AAA66817.1; -.
PIR; G46335; G46335.
HIV; M34193; ENV$OMVVSACG.
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Viruses; Retroid
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ENV polyprotein precursor (Coat polyprotein).
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Virology 175:434-447(1990).
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Querat G., Audoly G., Sonigo P., Vigne R.;
"Nucleotide sequence analysis of SA-OMVV, a visna-rollection sequence analysis of lentiviruses.";
lentivirus: phylogenetic history of lentiviruses.";
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P35581; P11525; P11526;
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harr Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Davies R., Murphy L., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.; Nature 393:537-544(1998).
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EMBL; AE007012; AAK45661.1;
TIGR; MT1398; --
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01-OCT-1996 (Rel. 34, Last sequence)
15-JUN-2002 (Rel. 41, Last annotat.
Hypothetical protein Rv1355c
RV1355C OR MT1398 OR MTCY02B10.19C
                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contents to the content is not removed.
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STRAIN=CDC 1551 / Oshkosh;
                                                                                                                                                                                                                                 Hypothetical protein; Complete proteome. SEQUENCE 715 AA; 78181 MW; 455495248A56041C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Peterson J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg Belcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium
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01-OCT-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Whole genome comparison of laboratory strains.";
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NCBI_TaxID=1773;
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OR RV3580C OR tuberculosis. synthetase

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MEDLINE=93223697; PubMed=8467807;
Casteels-Josson K., Capaci T., Casteels P.,
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Insecta; Pterygota; Neoptera; Endopterygota;
Aculeata; Apodea; Apidae; Apis.
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% S06675; S06675.
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Antibiotic;
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residues; Repeat.
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1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                            Score 54;
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des from honeybees.
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                      CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBI outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  laboratory strains:";
Submitted (ARR-2001) to the EMBL/GenBank/DDBJ databases.
Sibmitted (ARR-2001) to the EMBL/GenBank/DDBJ databases.
-:- CATALYTIC ACTIVITY: ATP + L-cysteine + tRNA(Cys) = AMP + diphosphate + L-cysteinyl-tRNA(Cys).
-:- SUBGUNIT: MONOMER (BY SIMILARITY).
-:- SUBGUNIT: MONOMER (BY SIMILARITY).
-:- SUBCELLULAR LOCATION: Cytoplasmic.
-:- SUMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
STRONG, TO METHIONYL-TRNA SYNTHETASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002308; Cys_tRNA-syn
InterPro; IPR001411; tRNA-synt_I:
Pfam; Pf01406; tRNA-synt_le; 1.
PRINTS; PR00983; TRNASYNTHCYS.
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                                                                                                                                                                                                                                                                                                                                                                                                                BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGRFAMS; TIGRO0435; cysS; 1.
PROSITE; PS00178; AA_TRNA_LIGASE_I;
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                                                                                                                         PWWEWAATHERAFTAAYDALDVLPPSAEP 117
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                                                                                                                                                                                                                                      0;
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Pred. No.
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ATP (BY SIMILARITY).
D -> E (IN REF. 2).
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15-JUL-1999
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P57990;
16-OCT-2001
16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                  BINDING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N., Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M., Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Cysteinyl-tRNA synthetase 1 (EC 6.1.1.16) (Cysteine--tRNA ligase
CYSES 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Squares S., S. Barrell B.G.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGRFAMS; TIGR00435; cyss; 1.
PROSITE; PS00178; AA_TRNA_LIGASE_I; FALSE_NEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 409:1007-1011(2001).
-!- CATALYTIC ACTIVITY: ATP + L-cysteine +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Massive gene decay in the leprosy bacillus.";
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InterPro; IPR001412; tRNA-synt_I.
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SUBUNIT: MONOMER (BY SIMILARITY).
SUBCELLULAR LOCATION: CYCOPIasmic.
SIMILARITY: BELONGS TO CLASS-I ĀMINOACYL-TRNA SYNTHETASE FAMILY.
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                                                                                                       STANDARD;
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ATP (BY
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Pred. No.
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TP (BY SIMILARITY).
9FD6CF859C69316D CRC64;
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MEDLINE=90264837; PubMed=2345367;
Raabe T., Schelle-Prinz B., Siddell S.G.
"Nucleotide sequence of the gene encodin
human coronavirus HCV 229E.";
J. Gen. Virol. 71:1065-1073(1990).
-1- FUNCTION: THE PEPLOMER PROTEIN MEDIA
TO THE HOST CELL RECEPTOR AND IS INV
AND IN SYNCYTIUM FORMATION.
                                                                                                              CARBOHYD
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                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                     Glycoprotein;
                                                                                                                                                                                                                                                                                                           Pfam; PF01600; Corona_S1;
Pfam; PF01601; Corona_S2;
                                                                                                                                                                                                                                                                                                                                           PIR;
                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                    · 1 - SUBCELLULAR LOCATION: Type I membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE=90264837;
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Coronaviridae; Co
NCBI_TaxID=11137;
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Local
       Match
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Similarity
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IPR002552; Corona_S2.
                       positive-strand Coronavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                precursor
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22.4%;
                      128639
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CYTOPLASMIC |
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Score
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EXTRACELLULAR (POTENTIAL).
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InterPro; InterPro; InterPro; InterPro; InterPro;

D; IPR001314; Chymotry;
D; IPR000024; Fz\_domain
D; IPR0002172; LDL\_recept
D; IPR01254; Ser\_prot(D); IPR001190; Srcr\_recept\_a;
D; IPR001190; Srcr\_recept\_a;

; Fz\_domain. ; LDL\_recept\_A. ; Ser\_protease\_Try. ; Srcr\_receptor. recept\_a; 6.

Chymotrypsin

MIM;

605236;

MEROPS;

S01.019;

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RESULT
CORI_HU
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O9Y5Q5; Q9UHY2;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence upda
15-JUN-2002 (Rel. 41, Last annotation up
Atrial natriuteric peptide-converting en
converting enzyme) (Corin) (Heart specif
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                                                    entities
or send a
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Proc. Natl. Acad. Sci. U.S.A. 97:8525-8529(2000)
-i- FUNCTION: CONVERTS PRO-ANP TO ANP. CLEAVES P
BETWEEN ARG-123 AND SER-124.
-i- SUBCELLULAR LOCATION: Type II membrane prote
-i- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEAR
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   EMBL;
HSSP;
                                                                                                          between the Swiss Institute of Bioinformatics Institute. The European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
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Mammalia; Eutheria;
                                                                                                use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20359740; PubMed=10880574; Yan W., Wu F., Morser J., Wu Q.;
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                                                                                                                                                                                           SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
SIMILARITY: CONTAINS 7 LDL-RECEPTOR CLASS A
SIMILARITY: CONTAINS 2 FRIZZLED (FZ) DOMAINS
SIMILARITY: CONTAINS 1 SRCR DOMAIN.
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AAF21966.1;
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man A.L., Clarke
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Primates;
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Pfam; PF00089; Pfam; PF01392;

trypsin; Fz; 2.

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PRINTS; PR00261; LDLRECEPTOR.
SMART; SM00063; FRI; 2.
SMART; SM00192; LDLa; 7.
SMART; SM00202; SR; 1.
SMART; SM00202; Tryp_SPC; 1.
PROSITE; PS50038; FZ; 2.
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PS50068;
PS50240;
PS00134;
PS00135;
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                                              Similarity 36.9; Conservative
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TRYPSIN_SER; 1.
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SRCR_2; FALSE_NEG.
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CHARGE RELAY SYSTEM.
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K -> R (IN REF. 2).
MW; 7705398EBB607AD2 CRC64;
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CORI_MOUSE
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PRINTS; PR007261; LDLRECEPTOR.
SMART; SM00063; FRI; 2.
SMART; SM00063; FRI; 2.
SMART; SM00102; SR; 1.
SMART; SM001020; Tryp_SPc; 1.
SMART; SM00020; Tryp_SPc; 1.
SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS50038; FZ; 2.
PROSITE; PS50068; LDLRA_1; 6.
PROSITE; PS50068; LDLRA_2; 7.
PROSITE; PS50068; LDLRA_2; 7.
PROSITE; PS500420; SRCR_1; FALSE_NEG.
PROSITE; PS500240; TRYPSIN_DOM; 1.
PROSITE; PS500240; TRYPSIN_HIS; FALSE_N
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16-OCT-2001 (Rel. 40, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
Atrial natriuteric peptide-converting enzyme (EC 3.4.21.-) (pro-ANP-converting enzyme) (Corin) (Low density lipoprotein receptor related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. The use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See J
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SEQUENCE FROM N.A.

MEDLINE-98429596; PubMed=9756624;

Tomita Y., Kim D.-H., Magoori K., Fujino T., Yamamoto T.T.;

Tomita Y., Kim D.-H., Magoori R., Fujino T., Yamamoto T.T.;

"A novel low-density lipoprotein receptor-related protein with

"A novel low-density lipoprotein abundant in heart.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein 4)
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Mammalia; Eutheria;
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InterPro; IPR000024; Fz_domain.
InterPro; IPR002172; LDL_recept_A.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR001190; Srcr_receptor.
pfam; PF00057; ldl_recept_a; 6.
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                                                                                    Hydrolase;
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Metazoa; Rodentia; S
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01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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"Cloning of a higher-plant plastid omega-6 fatty acid desaturase cDNA and its expression in a cyanobacterium.";

Plant Physiol. 105:635-641(1994).

-i- FUNCTION: CHLOROPLAST OMEGA-6 FATTY ACID DESATURASE INTRODUCES THE SECOND DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.

-i- PATHWAY: Polyunsaturated fatty acid biosynthesis.
                                                                                                                                                                                                                                                                                                                                                     Glycine max (Soybean).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Roside seurosids I; Fabales; Fabaceae; Papillonoideae; Phaseoleae; Glycine
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                                                                                                                                                                                                          Pfam; PF00487; FA_desaturase; 1. ProDom; PD001081; FA_desaturase; 1.
                                                                                                                                                                                                                                    EMBL; L29215; AAA50158.1; -.
InterPro; IPR001225; FA_desaturase.
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                                                                                                       SEQUENCE
                                                                                                                                                                                              Oxidoreductase; Fatty acid
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YPYEPWRFKHDRH-HAKTNMLREDTAWHPVWK
                        WPWWPWRRKHEAEPEAEPIMILKKWPWWP-WR
                                                   11;
                                                                                                                                                                                  peptide.
                                                                Similarity
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201
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OMEGA-6 FATTY ACID DESATURA
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Search completed: January 15, 2003, 18:08:53 Job time : 13 secs

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(c) 1993 - 2003
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	hypothetical prote	hypothetical próte	transcription fact	hypothetical prote	chloramphenicol O-	H+-transporting tw	capsid polyprotein	glycine cleavage s	hypothetical prote	Shb-like adapter p	omega-6 desaturase	coenzyme F420-redu	hypothetical prote	low-density lipopr	hypothetical prote

### ALIGNMENTS

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C;Species: Bos primigenius taurus (cattle)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: JC1222; A42387; S2564
R;del Sal, G.; Storici, P.; Schneider, C.; Romeo, D.; Zanetti, M.
Blochem. Biophys. Res. Commun. 187, 467-472, 1992
A;Title: cDNA cloning of the neutrophil bactericidal peptide indolicidin.
A;Reference number: JC1222; MUID:92392388; PMID:1520337
A;Accession: JC1222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A:Molecule type: protein
A;Residues: 131-143 <SEL>
A;Residues: 131-143 <SEL>
A;Residues: 131-145 <SEL>
A;Experimental source: neutrophils
A;Note: sequence extracted from NCBI backbone (NCBID:83840)
C;Superfamily: cathelin; cystatin homology
C;Keywords: amidated carboxyl end
E;1-29/Domain: signal sequence #status predicted <SIG>
E;22-129/Domain: cystatin homology <CYS>
                                                                                                                                                                                                    RESULT
H86543
                                                                                                                                                                                                                                                                                                                                               20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;22-129/Domain: cystatin homology <CYS>
F;30-130/Domain: propeptide #status predicted <PRO>
F;131-143/Product: indolicidin #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:X67340; NID:g462; PIDN:CAA47755.1; PID:g463
A;Experimental source: bone marrow
R;Selsted, M.E.; Novotny, M.J.; Morris, W.L.; Tang, Y.Q.; Smith, W.; Cullor, J.S.
J. Biol. Chem. 267, 4292-4295, 1992
A;Title: Indolicidin, a novel bactericidal tridecapeptide amide from neutrophils.
A;Reference number: A42387; MUID:92165771; PMID:1537821
A;Accession: A42387
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A; Residues: 1-144 <SAL>
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-314 <LIO>
A;Cross references: EMBL
A;Note: the authors trans
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C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
C;Accession: D72081; G81589
R;Kalman, S; Mitchell, W; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; (Nature Genet. 21, 385-389, 1999
                                                                                                                                                                                                                                                                                                                                        hypothetical protein 3 - Bacillus stearothermophilus
c;Species: Bacillus stearothermophilus
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 15-Oct-1999
C;Accession: S43916
R;Liong, E.C.; Ferenci, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNANA;Residues: 1-192 <ARNAPA;Residues: 1-192 <ARNAPA;Residue
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-192 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:AE002195; GB:AE002161; NID:g7189246; PIDN:AAF38182.1; PID:g718925
A;Experimental source: strain AR39, HL cells
C:Genetics:
A;Gene: CPn0426; CP0327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  conserved hypothetical protein frameshifted CP0327 [imported] - Chlamydophila N,Alternate names: hypothetical protein CT277 homolog
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                                                                                                                                                                                            A; Title: Molecular cloning of a maltose transport gene from A; Reference number: $43914; MUID:94247374; PMID:8190087 A; Accession: $43916
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A; Residues: 1-192 < REA>
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                                                                                                                                                                                                                                                                                                                erenci, T.
243, 343-352, 1994
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    EMBL:L13418; NID:g436964; translated the initiation
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42.3%;
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42.3%;
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    PIDN:AAA71981.1; PID:g436967 codon GTG for residue 1 as Val
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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                                            genome polyprotein - encephalomyocarditis virus N;Contains: coat protein VP1; coat protein VP2; coat protein EC 3.4.-.); RNA-directed RNA polymerase (EC 2.7.7.48) C;Species: encephalomyocarditis virus, EMCV
                                                                                                                                                                                                        GNNYE
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hypothetical protein SCE36.09 - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999 C;Accession: T36208 R;Oliver, K; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajanc submitted to the EMBL Data Library, May 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:AE005673; NID:g13423210; PIDN:AAK23758.1; GSPDB:GN00148 C;Genetics: A;Gene: CC1782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kon, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, Cproc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein CC1782 [imported] - Caulobacter crescentus C;Species: Caulobacter crescentus C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001 C;Accession: B87470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QY
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Best Local Similarity
Thehes 17; Conserv
                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-114 <OLI>
A; Cross-references: EMB
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A; Residues: 1-381 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Title: Complete Genome Sequence of Caulobacter crescentus. A; Reference number: A87249; MUID:21173698; PMID:11259647
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                              QУ
                                                                                                                                                                                                                                                                               A; Reference number: Z21601
A; Accession: T36208
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                                                                                                                                               A; Gene:
                                                                                                                                                                                                                                                           A; Status: preliminary; translated from
                                                                                                                                                                                  A; Experimental source: strain
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                                                                                                      Query Match
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                                                                         Matches
                                                                                         Best Local Similarity
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93
                                  18 PEAEPIMILKKW-PWWPWRR
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                                                                                                                                               SCOEDB: SCE36.09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WWPRRGGWRKALQMKPRAAPLRKLYDW 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WWP----WRRKHEAEPEAEPIMILKKW 29
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PETAPADAARRWRPRWPWRR 112
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                                                                     Conservative
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ce: strain A3(2)
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34.7%;
                                                                                         24.7%;
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                                  36
                                                                       2;
                                                                                         Score
Pred.
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Pred. No.
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Pred.
                                                                                                                                                                                                       PIDN:CAB42078.1; GSPDB:GN00070; SCOEDB:SCE36.09
                                                                                                                                                                                                                                                                                                                 S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, May 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                         Mismatches
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                                                                                         59.5;
No. 1
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No.
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2.3;
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                                                                                                          Length 114;
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host Homo

sapiens

(man)

VΡ3;

coat

protein

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A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E. C.A.; Li, J.H.; Li, Y.; Lin, X.; Lin, S.X.; Lin, Z.A.; Luros, J.S.; Maiti, R.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: E86447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;1057-1192/Product: core protein P2-B #status predicted <P2B>F;1193-1517/Product: core protein P2-C #status predicted <P2C>F;1193-1517/Product: core protein P3-A #status predicted <P3A>F;1518-1605/Product: core protein P3-A #status predicted <P3A>F;1606-1625/Product: genome-linked protein VPg #status predicted <VF;1626-1830/Product: proteinase #status predicted <PTS>F;1831-2290/Product: RNA-directed RNA polymerase #status predicted
                                                                                                                    A; Gene
A; Map
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F;392-622/Product: coat protein VP3 *status predicted <VP3>
F;623-910/Product: coat protein VP1 *status predicted <VP1>
F;621-1056/Product: core protein P2-A *status predicted <P2A>
F;911-1056/Product: core protein P2-A *status predicted <P2A>
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A;Note: the authors translated the codon CAU for residue 713 as Thr and AAC for residue C;Superfamily: foot-and-mouth disease virus genome polyprotein C;Keywords: coat protein; core protein; genome-linked protein; hydrolase; nucleotidyltra F;1-67/Domain: leader peptide #status predicted <LDP>
F;68-136/Product: coat protein VP4 #status predicted <VP4>
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                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-95 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, (Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; ansen, N.F.; Hughes, B.; Hulzar, L. Nature 408, 816-820, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein F5D14.5 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
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A; Residues: 1337-1396,'L',1398-1517,'A',1519-1536,'E',1538-1556,'S',1558-1611,'T',1613-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Palmenberg, A.C.; Kirby, E.M.; Janda, M.R.; Drake, N.L.; Duke, Nucleic Acids Res. 12, 2969-2985, 1984
A;Title: The nucleotide and deduced amino acid sequences of the ear, Reference number: A03906; MUID:84169586; PMID:6324136
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C; Accession: A03906; JN0383
                                                                                                                                                                                                          A;Cross-references:
                                                                                                                                                                                                                                                                                          A; Status: preliminary
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A; Residues: 1-2290 < PAL>
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                                                                                                                                                                         Genetics:
                                Query Match
Best Local
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10; Conserv
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           Conservative
                                                                                                                                                                                                       GB:AE005172;
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26.2%;
                                24.5%;
  Score 59; DB Pred. No. 1.6; 5; Mismatches
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Pred. No. 38
     5
                                                                                                                                                                                                          NID: 98920603;
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                          DB
1.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                       PIDN: AAF81325.1;
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     4.
                                                        Length 95;
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     Indels
                                                                                                                                                                                                       GSPDB:GN00141
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     28;
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Gaps
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 19-Mar-1997 #sequence\_revision 17
C;Accession: S21976
R;Kahre, O.; Ilves, H.; Speek, M.

17-Oct-1997

#text\_change

26-Aug-1999

2.7.7.49)

(clone

MH2C)

rat retrotransposon

Ilves, H.; Speek,

Library,

August 1991

probable RNA-directed DNA polymerase (EC N; Alternate names: reverse transcriptase

S21976

В

79

RKWPWSKPERPSAAEPDATP

98

0

A; Reference number: S16783 A; Accession: S21976

submitted to the EMBL Data

A; Molecule type:

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DNA Res.
A; Title:
                                                                                                                                                                                                                                                                 hypothetical protein SC6G9.38 - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Species: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-485 <KAN>
A; Cross-references: EMBL:D90901;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Synechocystis
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequ
C;Accession: S74708
Qγ
                                                                                       A; Gene:
                                                                                                       A; Experimental source: strain C; Genetics:
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                                                                                                                                       A; Cross-references:
                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-107 <SEE>
                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                             A; Reference number: A; Accession: T35634
                                                                                                                                                                                                                          R;Seeger, K.J.; Harris, D.; James, K.D.; submitted to the EMBL Data Library, June
                                                                                                                                                                                                                                                        C; Accession:
                                                                                                                                                                                                                                                                                                                   T35634
                                                                                                                                                                                                                                                                                                                                 RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Note:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R; Kaneko,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein slr1306 -
                             Query Ma
Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    K.; Okumura, S.; Shimpo, S.;
K.; Okumura, S.; Shimpo, S.;
A Res. 3, 109-136, 1996
Title: Sequence analysis of th
                                                                                                                                                                                                                                                                                                                                                                             41 PWDQWGLWALSGLGLVIWRWRRRHHAPPEQKQMLTPEVLQK
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                                             Local
   ω
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the nucleotide
                                                                                         SCOEDB: SC6G9.38
 KKWPWWPWRRKHEAEPEAEP
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12; Conser
                               l Similarity
10; Conserv
                                                                                                                                                                                                                                                         T35634
                                Conservative
                                                                                                                                                                                                             221584
                                                                                                                     EMBL:AL079356;
ce: strain A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence
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                                           24.1%;
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22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; GB:AB001339;
was submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H.; Tanaka, A.; Asamizu, Takeuchi, C.; Wada, T.;
                               2,
                                             Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 59; DB
Pred. No. 8.6;
                                                                                                                                     PIDN:CAB45629.1;
                                                                                                                                                                                                                          K.D.; Parkhill,
June 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                Mismatches
                                             No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the unicellular cyanobacterium Synechocys
                                          2.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NID:g1651897; PIDN:BAA16859.1; to the EMBL Data Library, June
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 485;
                                                                                                                                     GSPDB:GN00070;
                                                                                                                                                                                                                                                                                                                                                                               18
                                                                                                                                                                                                                                                                                                                                                                                                          28
                                                           Length
                                Indels
                                                                                                                                                                                                                                         Barrell,
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                                                                                                                                                                                                                                         в.G.;
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                             Gaps
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PID:d101 1996

2

3

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A; Molecule type: DNA
A; Residues: 1-376 <SEE>
A; Cross-references: EMBL; AL035216; PIDN:CAA22819.1; GSPDB:GN00067; SPDB:SPBC646.15c
A; Experimental source: strain 972h-; cosmid c646
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residues: 1-513 <KAH>.
A; Cross-references: EMBL: X61295; |
A; Experimental source: clone MH2C
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Superfamily: pol polyprotein
C; Keywords: nucleotidyltransferase; polyprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: Z21938
A; Accession: T40591
A; Status: preliminary; tran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 04-Mar-2000
C;Accession: T40591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
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RESULT 14
T28094
                                                                                                                                                                                                                                                               cell 66, 769-780, 1991
A;Title: The act cluster contains regulatory and antibiotic export genes, direct targets A:Reference number: A40046; MUID:91347376; PMID:1878971
A;Accession: C40046
                                                                                                                                                                                                                                                                                                                                                 antibiotic transport-associated protein actII-3 - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 22-Oct-19: C;Accession: C40046
                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
C40046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Map position: 2
A; Introns: 49/1; 126/2; 312/2; 350/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, submitted to the EMBL Data Library, January 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical
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                                                                   Дδ
                                                                                                   2
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A;Residues: 1-711 <FER>
A;Cross-references: GB:M64683; NID:g153143;
                                                                                                                                                                                                                                                                                                                                   R; Fernandez-Moreno, M.A.; Caballero,
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                                                                     332 IFGRWVFWPARPKHGTEPD 350
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13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 37.0
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                                                                                                                                       Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schizosaccharomyces pombe hypothetical protein SPBC646.15c
                                                                                                                                       23.7%;
nilarity 47.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL: X61295; NID: g56521; PIDN: CAA43593.1; PID: g56522
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Pred. No.
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Pred. No. 1
                                                                                                                                                            Score 57; DB Pred. No. 23;
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12;
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Search completed: January Job time: 21 secs

15,

2003,

18:09:54

Вр

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hypothetical protein ZK899.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
C;Accession: T28094
                                                                                                                                                                                                                                                                                                                                                                                                           myosin heavy chain - fluke (Schistosoma mansoni) (fragment)
N;Alternate names: surface antigen, 200K
C;Species: Schistosoma mansoni
C;Species: Schistosoma mansoni
C;Date: 22-Nov-1993 #sequence_revision 06-Sep-1996 #text_change 13-Feb-1998
C;Accession: S33068
                                                                                                                                                                    A;Cross-references: EMBL:X65591
A;Note: the authors translated the
C;Superfamily: myosin heavy chain;
C;Keywords: ATP; surface antigen
                                                                                                                                                                                                                                                                                                                      R;Soisson, L.M.A.; Masterson, C.P.; Tom, T.D.; McNally, M.T.; Lowell, G.H.; Strand, M. T. Immunol. 149, 3612-3620, 1992.
J. Immunol. 149, 3612-3620, 1992.
A;Title: Induction of protective immunity in mice using a 62-kDa recombinant fragment A;Title: Induction of protective immunity in Mice using a 62-kDa recombinant fragment A;Reference number: A46514; MUID:93056536; PMID:1431131
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A; Introns: 34/3; 143/2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-452 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary; translated from GB/EMBL/DDBJ
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A; Reference number: Z20468
A; Accession: T28094
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                                      δã
                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-527 <SOI>
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106 VLRNWPWWRLYTKVKPMLNIARQEEEMKKAAEELAKLKE
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les 10; Conser
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                                      1 ILKKWPWW-----PW----RRKHEAEPEAEPIMILKK
                                                                                    12;
                                                                                                           Similarity
                                                                                    Conservative
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Pred. No.
                                                                                                           Score 55.5;
Pred. No. 25;
                                                                                                                                                                                             codon CAA for residue 346 as myosin motor domain homology
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                                                                                         Mismatches
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hypothetical protein ZK899
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19;
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Perfect score:
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137.5
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Published_Applications_AA:*

1: /cgn2_6/ptodata/1/pubpaa/Pi
2: /cgn2_6/ptodata/1/pubpaa/Pi
3: /cgn2_6/ptodata/1/pubpaa/Ui
4: /cgn2_6/ptodata/1/pubpaa/Ui
6: /cgn2_6/ptodata/1/pubpaa/Ui
6: /cgn2_6/ptodata/1/pubpaa/Ui
7: /cgn2_6/ptodata/1/pubpaa/Ui
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10: /cgn2_6/ptodata/1/pubpaa/Ui
11: /cgn2_6/ptodata/1/pubpaa/Ii
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Maximum Match 100%
Listing first 45 summaries
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: /cgn2_6/ptodata/1/pubpaa/JCTUS_PUBCOMB.pep:*
: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
1: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
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US-09-030-619-50
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US-09-030-619-47
US-09-030-619-47
US-09-030-619-47
US-09-030-619-112
US-09-030-619-53
US-09-030-619-53
US-09-030-619-54
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66.864 Million cell updates/sec
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Sequence
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104 App
50, Appl
69, Appl
52, Appl
51, Appl
99, Appl
108, Appl
110, Appl
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SULT 1  Sequence 104, Application Sequence 104, Application GENERAL INFORMATION:  APPLICANT: Krieger, Timo APPLICANT: Taylor, Rober APPLICANT: Fraser, Jonet APPLICANT: West, Michael APPLICANT: Monicol, Patr TITLE OF INVENTION: INFORMATION: COMP		45	44	43	42	41	9	38	37	36	35	34	33	32	ω c		) N	27	26	25	24	23	22	21	20	
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9-104 04, Application US20020035061A1 FORMATION: CATINGER, Timo Taylor, Rober Exfle, Dougla Fraser, Janet West, Michael Fraser, West, Michael CHONNION: COMP INVENTION: COMP		30.3	30.3	30.5	30.5	31. 1.		31.5	32.0	32.2	32.4	32.4	32.4	33.6	ω . σ .	3 4 . 0 .	34.0	34.0	34.2	34.4	34.4	34.4	34.4	34.6	35.3	
ation US/09030 5061A1 , Timothy J. Robert Douglas Janet R. Janet R. Jichael H.P. , Patricia J. , Patricia J. COMPOSITIONS U		10	ٰ و			12																				
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METHODS FOR TREATING	ALIGNMENTS	30-619	30-6	30-619-7	030-619-75	-619-1	030-619-23	030-619-82	030-619-42	030-619-40	030-619-43	030-619-113	030-619-78	030-619-114	030-619-79	030-619-34	030-619-59	030-619-58	030-619-48	030-619-24	30-6	6	30-6	30-619	619-	
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TITLE OF INVENTION: INFECTIONS USING CATIONI
TITLE OF INVENTION: WITH ANTIBIOTICS
FILE REFERENCE: 660081.406
CURRENT APPLICATION NUMBER: US/09/030,619B
CURRENT FILING DATE: 1998-02-25
NUMBER OF SED ID NOS: 232
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 104
LENGTH: 28
TYPE: PRT
         RESULT 2
US-09-030-619-50
US-09-030-619-50
; Sequence 50, Application US/09030619B
; Patent No. US20020035061A1
; GENERAL INFORMATION:
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Best Local
 APPLICANT:
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20; Conser
Krieger, Timothy J.
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US-09-030-619-52
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SEQ ID NO 50
LENGTH: 28
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Best Local S
Matches 21
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LENGTH: 21
TYPE: PRT
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Patent No. US20020035061A1
          Sequence 52, Application US/09030619B Patent No. US20020035061A1 GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/09/030,619B
CURRENT FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 232
SOFTWARE: FASTSEQ for Windows Version 3.0
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APPLICANT: West, Michael H.P.
APPLICANT: West, Michael H.P.
APPLICANT: West, Michael H.P.
APPLICANT: West, Michael R.P.
TITLE OF INVENTION: COMPOSITIONS USING TITLE OF INVENTION: WITH ANTHHOTICS
FILE REFERENCE: 660081.406
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APPLICANT:
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Best Local Similarity
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APPLICANT: MCNICOL, Patricia J.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALC
TITLE OF INVENTION: WITH ANYIBIOTICS
                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/030,619B
CURRENT FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 232
SOFTWARE: FastSEQ for Windows Version 3.0
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APPLICANT:
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Erfle, Douglas
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Erfle, Douglas
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64.38;
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Pred. No. 4.7e-06;
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, OTHER INFORMATION: Indolicidin Analogue US-09-030-619-52
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RESULT 6
US-09-030-619-95
Sequence 95, Application User 100, 0820020035061A1
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SEQ ID NO 52
LENGTH: 21
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Best Local :
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SEQ ID NO 51
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
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APPLICANT: Fraser, Janet R.
APPLICANT: West, Michael H.P.
APPLICANT: West, Michael H.P.
APPLICANT: McNicol, Patricia J.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR
TITLE OF INVENTION: WITH ANTIBIOTICS
FILE REFERENCE: 660081.406
FILE REFERENCE: 660081.406
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APPLICANT:
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Best Local Similarity
Matches 17; Conserv
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APPLICANT: West, Michael H.P.
APPLICANT: McNicol, Patricia J.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
TITLE OF INVENTION: WITH ANTIBIOTICS
FILE REFERENCE: 660081.406
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                                                                                                                 1 ILKKWPWWPWRR------
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o. US20020035061A1
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Erfle, Douglas
Fraser, Janet R.
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                         Application US/09030619B
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Pred. No. 6.1e-06;
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Pred. No. 2
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GENERAL INFORMATION:

APPLICANT:

Taylor, Erfle, D

Krieger, Timothy J. Taylor, Robert

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US-09-030-619-72
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                                                                                                                                        RESULT 8
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US-09-030-619-99
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CURRENT FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 95
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                    GENERAL INFORMATION:
            APPLICANT:
APPLICANT:
APPLICANT:
                                                                                    Sequence 72, Application US/09030619B Patent No. US20020035061A1
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Best Local :
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APPLICANT: West, Michael H.P.
APPLICANT: MCNICOL, Patricia J.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: WITH ANTHODTICS
FILE REFERENCE: 660081.406
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TITLE OF INVENTION: COMPOSTITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALC
TITLE OF INVENTION: WITH ANTIBIOTICS
FILE REFERENCE: 660081.406
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SOFTWARE: FastSEQ for Windows Version
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APPLICANT:
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TYPE: PRT
ORGANISM: Artificial Sequence
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1 ILKKWPWWPWRRK 13
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13; Conserv
            Krieger, Timothy J.
Taylor, Robert
Erfle, Douglas
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Erfle, Douglas
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Pred. No.
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Pred. No.
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hes 0;
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RESULT 10
US-09-030-619-47
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LENGTH: 14
TYPE: PRT
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CURRENT FILING DATE: 1998-02-25
CURRENT FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 232
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 108
LENGTH: 14
Sequence 47, Application US/09030619B Patent No. US20020035061A1
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INPECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
TITLE OF INVENTION: WITH ANTIBIOTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/030,619B
CURRENT FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 232
SOFTWARE: FastSEQ for Windows Version 3.0
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Erfle, Douglas
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Pred. No.
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2.7e-05;
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GENERAL INFORMATION: APPLICANT: Krieger

APPLICANT:

Krieger, Timothy J. Taylor, Robert Erfle, Douglas

APPLICANT:

Fraser, Janet R. West, Michael H.P.

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RESULT 12
US-09-030-619-112
; Sequence 112, Application US/09030619B
; Patent No. US20020035061A1
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CURRENT FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 47
LENGTH: 21
TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Whiches 12; Conservative
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SOFTWARE: FastSEQ for
SEQ ID NO 67
LENGTH: 12
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TITLE OF INVENTION: WITH ANTIBIOTICS
TITLE REFERENCE: 660081.406
PTI.E REFERENCE: 660081.406
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS USING CATIONIC PRPTIDES ALG
TITLE OF INVENTION: WITH ANTIBIOTICS
FILE REFERENCE: 660081.406
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Erfle, Douglas
Fraser, Janet R.
West, Michael H.P.
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                                               Krieger, Timothy J. Taylor, Robert Erfle, Douglas
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               Fraser, Janet R. West, Michael H.P.
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                                                                                                                                                                                                                                                                                                                               Score 87; DB 10; Pred. No. 6.7e-05;
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Pred. No. 0.0001;
1; Mismatches 0;
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; OTHER INFORMATION: Cationic Peptide US-09-030-619-112
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                                                                GENERAL INFORMATION:
APPLICANT: Krieger,
APPLICANT: Taylor, F
APPLICANT: Erfle, Dc
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; OTHER INFORMATION: Indolicidin Analogue
US-09-030-619-53
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APPLICANT: West, Michael H.P.

APPLICANT: McNicol, Patricia J.

TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: INFECTIONS USING CATIONI
TITLE OF INVENTION: WITH ANTIBIOTICS
FILE REFERENCE: 660081.406
CURRENT APPLICATION NUMBER: US/09/030,619B
CURRENT FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 232
COMMENT: TSOLETO FOR UNICOUS Version 3 0
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SEQ ID NO 53
FENGTH: 13
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SEQ ID NO 112
LENGTH: 12
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Best Local 9
                                                                                                                                      Sequence 107, Application US/09030619B Patent No. US20020035061A1
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APPLICANT:
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CURRENT APPLICATION NUMBER: US/09/030,619B
CURRENT FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 232
NUMBER OF SEQ ID NOS: 232
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Best Local
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TITLE
                                  APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
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les 12; Conserv
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OF INVENTION:
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12; Conserv
Taylor, Robert
Erfle, Douglas
Fraser, Janet R.
West, Michael H.P.
MCNicol, Patticia J.
MCNENTION: COMPOSITIONS F
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Erfle, Douglas
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                                                                                                    Krieger, Timothy
                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                 Score 86;
Pred. No.
                                                                                                                                                                                                                                                                                                                 Mismatches
     AND METHODS FOR TREATING
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TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
TITLE OF INVENTION: WITH ANTIBIOTICS
FILE REFERBERUE: 660081.406
CURRENT APPLICATION NUMBER: US/09/030,6198
CURRENT FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 232
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 107
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Cationic Peptide Analogue
US-09-030-619-107
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Search completed: January 15, 2003, 18:13:20 Job time : 11 secs
                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Cationic Peptide Analogue US-09-030-619-109
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US-09-030-619-109
                                                                                                                                                                  Query Match
Best Local S
Matches 12
                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows
SEQ ID NO 109
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 109, Application US/09030619B Patent No. US20020035061A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 35.7%; Score 86; DB 10; Best Local Similarity 41.9%; Pred. No. 9.5e-05; Matches 13; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Taylor, Robert
APPLICANT: Erfle, Douglas
APPLICANT: Erfle, Douglas
APPLICANT: Fraser, Janet R.
APPLICANT: West, Michael H.P.
APPLICANT: West, Michael H.P.
APPLICANT: MCNICOL, Patricia J.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
TITLE OF INVENTION: WITH ANTIBIOTICS
FILE REFERENCE: 660081.406
CURRENT FILING DATE: 1998-02-25
CURRENT FILING DATE: 1998-02-25
CURRENT FILING DATE: 1998-02-25
COURRENT FILING DATE: 1998-02-25
                                                                                                                                                                                          Local Similarity
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                                                                                                                                                                      Conservative
                                                                                                                                                                                        35.7%; Score 86; DB 10; 100.0%; Pred. No. 9.5e-05;
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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1: /cgn2_6/ptodata/1

2: /cgn2_6/ptodata/1

3: /cgn2_6/ptodata/1

4: /cgn2_6/ptodata/1

5: /cgn2_6/ptodata/1

6: /cgn2_6/ptodata/1
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length: 2000000000
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Copyright (c) 1993 - 2003 Compu
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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                         2003, 18:07:56; Search time 14 Seconds (without alignments) 77.761 Million cell updates/sec
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  US-09-099-631A-12
US-08-915-314-54
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US-08-915-314-63
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US-08-915-314-63
US-08-915-314-63
US-08-915-314-57
US-08-915-314-57
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US-08-915-314-52
US-08-915-314-52
US-08-915-314-54
US-08-915-314-35
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Sequence 54,
Sequence 55,
Sequence 55,
Sequence 62,
Sequence 63,
Sequence 63,
Sequence 64,
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Sequence 38,
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38, Appl
56, Appl
56, Appl
57, Appl
62, Appl
63, Appl
63, Appl
64, Appl
57, Appl
58, Appl
59, Appl
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GENERAL INFORMATION:
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45	44	43	42	41	40	39	38	37	36	35	34	S S	32	31	30	29	28
79	80	80	80	81	82	82	82	82	82.5	83	83	83	83	83	83	83	83.5
32.8	33.2	33.2	33.2	33.6	34.0	34.0	34.0	34.0	34.2	34.4	34.4	34.4	34.4	34.4	34.4	34.4	34.6
17	16	15	14	11	13	13	13	13	21	20	13	13	13	13	13	12	15
4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4
US-08-702-054B-42	US-08-702-054B-2	US-08-702-054B-41	US-08-702-054B-18	US-08-915-314-75	US-08-702-054B-33	US-08-915-314-67	US-08-915-314-66	US-08-915-314-25	US-08-915-314-48	US-08-915-314-47	US-08-702-054B-35	US-08-702-054B-31	US-08-702-054B-30	US-08-915-314-50	US-08-915-314-49	US-08-915-314-24	US-08-702-054B-39
Sequence 42, Appl	Sequence 2, Appli	•	Sequence 18, Appl	•	•	67,	•	-	-	•	-	-	-	-	•	Sequence 24, Appl	`

# ALIGNMENTS

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Query Match
Best Local Similarity
""trhes 22; Conservation
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                                                                                                                                                                                                                                                                                                                                                                  US-08-702-054B-38
                                                                                                                                                                                                                                          Patent No. 6191254
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Falls, Timothy J.
APPLICANT: Hancock, Robert E. W.
APPLICANT: Gough, Monisha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/099,631A
CURRENT FILING DATE: 1998-06-18
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 12
LENGTH: 63
TYPE: PRT
                                                                                                                                                                                                                                                                                                                            Sequence 38, Application US/08702054B Patent No. 6191254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Selsted, Michael E.
APPLICANT: Osapay, Klara
TITLE OF INVENTION: Crosslink-Stabilized Indolicidin Analogs
FILE REFERENCE: P-UC 3050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence FEATURE:
COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                             STREET: 42...
STREET: 42...
CITY: La Jolla
CTATE: CA
TSA
                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richa
STREET: 4225 Executive
                                                                                                                                                                                                  TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDES TITLE OF INVENTION: AND METHODS OF SCREENING FOR THE
                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                          COUNTRY: UZIP: 92037
                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 KWPWWPWRRM-----ARIAMILPWKWPWWPWRR 38
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Pred. No. 2.9e-10;
0; Mismatches 5
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US-08-915-314-54
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                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,314
FILING DATE: 20-AUG-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6180604tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REGISTRATION NUMBER: 39,317
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
                                 TELEFAX: (206) 682-6031 [NFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
                                                                                         REFERENCE/DOCKET NUMBER: 66
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING TITLE OF INVENTION: INFECTIONS USING ANALOGUES OF INDOLICIDIN NUMBER OF SEQUENCES: 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: 1: MOLECULE TYPE:
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LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/002,6
FILING DATE: 23-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Halle, Lisa A.
REGISTRATION NUMBER: 38,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 23-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/002,687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 2.0b CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Taylor, Robert APPLICANT: Erfle, Douglas
                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM CONTROL OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
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                   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ILKKWPWWPWRRKHEAEPEAEPIMILKKWPWWPWRRK 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ILKKWPW-------WPWWPWRRK 16
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                             Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    6300 Columbia Center, 701 Fifth Avenue
                   21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fraser, Janet R. West, Michael H.P. Krieger, Timothy J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IBM Compatible
SYSTEM: Windows 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEED and BERRY LLP
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43.2%;
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Pred. No. 1.2e-06;
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RESULT 5
US-08-915-314-55
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US-08-915-314-56
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Sequence 55, Application US/08915314
Patent No. 6180604
GENERAL INFORMATION:
APPLICANT: Fraser, Janet R.
APPLICANT: West, Michael H.P.
                                                                                                                                                                                                           Query Match
Best Local (
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APPLICANT: Fraser, Janet R.
APPLICANT: West, Michael H.P.
APPLICANT: Krieger, Timothy J
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                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 66
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6180604temburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/915,314 FILING DATE: 20-AUG-1997
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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STATE:
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Taylor, Robert
Erfle, Douglas
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64.38;
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Pred. No.
                                                                                                                                                                                                            Score 98; 1
Pred. No. 2
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2.5e-06;
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Best Local 9
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Patent No. 6180604
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                                                                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 66
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                        APPLICANT: Krieger, Timothy J.
APPLICANT: Taylor, Robert
APPLICANT: Erile, Douglas
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS USING ANALOGUES OF INDOLICE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
NAME: No. 6180604tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
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CORRESPONDENCE ADDRESS:
                SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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 APPLICATION NUMBER:
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                                                                                                                                       Washington
7: USA
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                                                                                                                                                                                                                                                                                                                                                  West, Michael H.P.
                                                                                                                                                                                                                                                                                                                                                                  Fraser,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Krieger, Timothy J.
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Erfle, Douglas
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US/08/915,314
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Pred. No. 8.8e-06;
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                                                                                                                                                                                          701 Fifth Avenue
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JS-08-915-314-62
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Best Local S
Matches 13
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GENERAL INFORMATION:
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                                                                                                                                                   TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/915,314
FILING DATE: 20-AUG-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6180604tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 660081.405
                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: West, Michael H.P.
APPLICANT: Krieger, Timothy J.
APPLICANT: Taylor, Robert
APPLICANT: Erfle, Douglas
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS USING ANALOGUES OF INDOLICI
NUMBER OF SEQUENCES: 90
                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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NAME: No. 6180604tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
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ADDRESSEE: SEED and BERRY LLP
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                                                                  FEATURE:
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TYPE: a
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CLASSIFICATION:
                OTHER INFORMATION:
                               NAME/KEY: Modified-site LOCATION: 1
                                                                                    TOPOLOGY:
                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
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                                                                                                                                      LENGTH:
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13; Conserv
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206) 682-6031
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37.8%; Score 91; 100.0%; Pred. No.
              /note= "D-Form of Isoleucine"
                                                                                                                                                                                                                                                                                                                                                                                      Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center, 701 Fifth Avenue
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US-08-915-314-63
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                                                              US-08-915-314-64
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            Sequence 64, Application US/08915314
Patent No. 6180604
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No.
                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 13; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: No. 6180604tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING TITLE OF INVENTION: INFECTIONS USING ANALOGUES OF INDOLICIDIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Erfle, Douglas
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                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                            FEATURE:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 20 CLASSIFICATION:
                                                                                                                                                                                                                                                            LOCATION: 13
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                            NAME/KEY:
                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
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Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                         amino acid
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                                                                                                                                                                                                                                                                                                                                                                         13 amino acids
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                                                                                                                                                                                                                                                                                            Modified-site
   Fraser, Janet R.
                                                                                                                                                                                                                                                                                                                            linear
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                                                                                                                                                                                                                                                                                                                                                                                                       63:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   660081.405
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                                                                                                                                                                                                   Score 91; DB 4;
Pred. No. 1.1e-C
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US-09-042-071-36
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Best Local :
                                                                                                                                                                                                                      Patent No. 6294372
                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                            Sequence 36,
                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Burian, Jan
APPLICANT: Kay, Willian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (206) 682-603 INFORMATION FOR SEQ ID NO:
                                                                              APPLICANT: KAY, WILLIAM W.
TITLE OF INVENTION: REPLICA-
TITLE OF INVENTION: SMALL C!
TITLE OF INVENTION: CONTROL
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY AGENT INFORMATION:
NAME: NO. 6180604tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 660081.405
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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ADDRESSEE: SEED and BERRY LLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
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les 13; Conserv
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                                                 STREET:
COUNTRY:
                  STATE: Washington
                                    CITY:
                                                                   ADDRESSEE:
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                                                                                                                                                                                                                                            Application US/09042071
                                                    6300 Columbia Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Erfle, Douglas
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 USA
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Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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                                                                      SEED and BERRY LLP
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20-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  682-6031
                                                                                                                      REPLICATION GENES AND GENE PRODUCTS FROM SMALL CRYPTIC PLASMIDS AND METHODS FOR CONSTRUCTING CONTROLLED-REPLICATION PLASMID VECTORS
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                                                      701 Fifth Avenue
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COMPUTER READABLE FORM:

MEDIUM TYPE:

Floppy disk

OPERATING SYSTEM:

IBM PC compatible SYSTEM: PC-DOS/MS-DOS

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US-08-915-314-57
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Best Local Similarity
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                                  TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO: 57:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
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APPLICANT:
APPLICANT:
                                                                   ATTORNEY/AGENT INFORMATION:
NAME: NO. 6180604tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 66081.405
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 661
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,071
FILING DATE: 13-MAR-1998
                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: West, Michael H.P.
APPLICANT: Krieger, Timothy J.
APPLICANT: Taylor, Robert
APPLICANT: Erfle, Douglas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                               APPLICATION NUMBER: US/08/915,314 FILING DATE: 20-AUG-1997 CLASSIFICATION: 424
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                     Washington
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100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Janet R.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       660081.407
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                                                                                                                                                                                                                                                                                                                                                                                                                        701 Fifth Avenue
                                                                                                                                                                                                                                                           Version #1.30
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1.1e-05;
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RESULT 12
US-08-702-054B-40
US-08-702-054B-40
; Sequence 40, Application US/08702054B
; Patent No. 6191254
; Patent No. 6191254
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US-08-915-314-57
RESULT 13
US-08-915-314-46
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Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/002,68
FILING DATE: 23-AUG-1995
ATTORNEY_AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 0742
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 619/678-5099 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRENY AFFLICATION NUMBER: US/08/102, US/08/102, US/08/103, US/08/102, US/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM COMPC-COMPUTER: IBM COMPC-COMPUTER: Windows 95

COPTWARE: FastSEQ for Windows Version 2.0b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: La Jolla
STATE: CA
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ZIP: 92037
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Fish & Richardson P.C. STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
                                                                                                                                             1 ILKKWPWWPWRR-----WW
                                                                                                                                                                                 1 ILKKWPWWPWRRKHEAEPEAEPIMILKKWPWW 32
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Pred. No.
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Pred. No. 2.4e-05
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Sequence 46, Application US/08915314
Patent No. 6180604
GENERAL INFORMATION:

APPLICANT:

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INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
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APPLICANT:
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MEDJUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/915,314
FILING DATE: 20-AUG-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6180604tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 660081.405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING TITLE OF INVENTION: INFECTIONS USING ANALOGUES OF INDOLICIDIN NUMBER OF SEQUENCES: 90
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           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                        APPLICANT: Fraser, Janet R.
APPLICANT: West, Michael H.P.
APPLICANT: Krieger, Timothy J.
APPLICANT: Taylor, Robert
APPLICANT: Taylor, Robert
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS USING ANALOGUES OF INDOLICIDIN
NUMBER OF SEQUENCES: 90
                                                                                                          COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity les 15; Conserv
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                                                                                                                                                             CITY: Seattle
STATE: Washington
                                                                                                                                         COUNTRY:
                                                                                                                                                                                                    STREET:
                                                                                                                                                                                                                         ADDRESSEE:
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Taylor, Robert
Erfle, Douglas
                                                                                                                                                                                                      6300 Columbia Center,
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                                                                                                                                                                                                                         SEED and BERRY LLP
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20-AUG-1997
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US/08/915,314
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                                                                                                                                                                                                         701 Fifth Avenue
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RESULT 15
US-08-915-314-74
; Sequence 74, Application US/08915314
; Patent No. 6180604
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                                                                  US-08-915-314-74
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Matches
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentID Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/915,314
FILING DATE: 20-AUG-1997
CLASSIFICATION: 424
ATTORNEY/ACENT INFORMATION:
NAME: No. 6180604tenburg Ph.D., Carol
RECISTRATION NUMBER: 39,317
REPERENCE/DOCKET NUMBER: 39,317
REPERENCE/DOCKET NUMBER: 660081.405
TELEPHONE: (206) 632-4900
TENTERNY. (206) 632-4900
Query Match
Best Local S
Matches 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                         TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Fraser, J
APPLICANT: West, Mic
APPLICANT: Krieger
APPLICANT: Taylor, F
APPLICANT: Erfle, Do
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: No. 6180604tenburg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: CÓMPOSITIONS AND METHODS FOR TREATING TITLE OF INVENTION: INFECTIONS USING ANALOGUES OF INDOLICIDIN
                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 05...
CTTY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: No. 6180604tenburg Ph.D., Carol REGISTRATION NUMBER: 39,317 REFERENCE/DOCKET NUMBER: 660081.405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY:
STATE:
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                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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                                                                                        TOPOLOGY:
                                                                                                       STRANDEDNESS:
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                                                                                                                                         LENGTH:
l Similarity
12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fraser, Janet R. West, Michael H.P.
                                                                                                                                           12 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Krieger, Timothy J.
Taylor, Robert
Erfle, Douglas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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                                                                                      linear
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- NO: 52:
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 35.7%; Score 86; DB 4; L
100.0%; Pred. No. 4.5e-05;
Live 0; Mismatches 0;
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Pred. No. 3.3e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 12;
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Conservative

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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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241
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Amino acid sequenc Indolicidin analog Poly-(Indol (1-13) Indolicidin fusion Antimicrobial cati Indolicidin analog Amino acid sequenc Indolicidin analog Amino acid sequenc Indolicidin analog	AAY91800 AAW66363 AAY44668 AAY571142 AAW12899 AAY24582 AAY91806 AAY24571 AAY91808 AAY24571	21 21 21 18 19 21 19 21 19	28 63 63 16 21 21 21 21 20 20	58.7 57.1 55.4 55.4 41.3 41.1 41.1 40.7 38.8	141.5 137.5 133.5 133.5 99.5 99.9 99.9 98.93.5	10 10 10 10 10
Description	ID	DB	Query Match Length DB	Query Match	Score	Result

45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11
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AAW27179	AAY91828	AAY24586	AAW12882	AAY91813	AAY24573	AAY91812	AAY91803	AAY24572	AAY24613	AAW12896	AAY91833	AAY24615	AAW12877	AAY91804	AAY24580	AAY91796	AAW66376	AAY24552	AAW13802	AAY91811	AAY24583	ABB81254	AAY91820	AAY91819 ,	AAY91818	AAY91774	AAY91773	AAY92795	AAY94495	AAW71690	AAW66378	AAY24609	28	AAY91807
Antimicrobial cati	Amino acid sequenc	Indolicidin analog	Antimicrobial cati	Amino acid sequenc	Indolicidin analog	m	Amino acid sequenc	Indolicidin analog	Indolicidin analog	۳.	Amino acid sequenc	Indolicidin analog	Antimicrobial cati	Amino acid sequenc	icidin	Amino acid sequenc	Cationic peptide o	Indolicidin analog	μ.	Amino acid sequenc	Indolicidin analog	CP11-NH2 antibacte	acid	acid	acid		Amino acid sequenc	Indolicidin analog	Œ	Cationic peptide M	Cationic peptide o	Indolicidin analog	Antimicrobial cati	Amino acid sequenc

## ALIGNMENTS

OULY 1 91800 AAY91800 standard; Peptide; 28 AA. AAY91800; 06-JUN-2000 (first entry) Amino acid sequence of cationic peptide MBI 11B20CN. Cationic peptide; tumour; pharmaceutical composition	Σ	×	Œ	×	DT	×	AC	×	IJ	AAY	RES
ON.	Cationic peptide; tumour; pharmaceutical composition; cance		Amino acid sequence of cationic peptide MBI 11B20CN.		06-JUN-2000 (first entry)		AAY91800;		AAY91800 standard; Peptide; 28 AA.	AAY91800	RESULT 1

carrounc pepride; tumour; pharmaceutical composition; cancer; treatment; leukaemia; polyoxyalkylene-modified; APO; lymphoma; multiple myeloma; breast; lung; ovary; cervix; uterus; skin; prostate; liver; colon; multidrug resistance multidrug resistance.

Synthetic.

WO9965506-A2

14-JUN-1999; 99WO-CA00552.

23-DEC-1999

12-JUN-1998; 98US-0096541.

(MICR-) MICROLOGIX BIOTECH INC.

Friedland HD, Krieger TJ, Taylor R, Erfle D, Fraser JR, West MHP;

WPI; 2000-223549/19.

Novel pharmaceutical composition containing optionally activated polyoxyalkylene-modified cationic peptides, useful for treating tumours

2;

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RESULT 2
AAW66363
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H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents a cationic peptide amino acid sequence, which can be used in the pharmaceutical composition of the invention. The invention relates to a pharmaceutical composition containing at least one activated polyoxyalkylene (APO) -modified cationic peptide. The modification of peptides with APO increases their activity against tumour ceils, including those with a multidrug resistant phenotype. The pharmaceutical composition can be used to treat tumours, specifically lymphoma, leukaemia, multiple myeloma, or tumours of breast, lung, ovary, cervix, uterus, skin, prostate, liver and colon.
                                                                                                                                                                                                                                                                                           25-FEB-1998;
10-MAR-1997;
20-AUG-1997;
26-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1;
          The present sequence represents an indolicidin analogue. The present invention describes compositions and methods for treating infection, especially bacterial infections. The compositions and methods use cationic peptides in combination with an antibiotic agent which are then administered to a patient to enhance the activity of the antibiotic agent, to overcome: (a) tolerance; (b) acquired resistance; and (c) inherent resistance. The combinations of antibiotics and cationic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                 New indolicidin peptide analogues - useful for, e.g. enhancing activity of antibiotic or overcoming tolerance, acquired resistance or inherent resistance of microorganisms
                                                                                                                                                                                                                                                                                                                                                                                          17-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW66363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW66363 standard;
                                                                                                                          Claim 1; Page 91; 105pp; English.
                                                                                                                                                                                                            WPI; 1998-520800/44
                                                                                                                                                                                                                                                               (MICR-) MICROLOGIX
                                                                                                                                                                                                                                                                                                                                                                10-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                    WO9840401-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indolicidin analogue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indolicidin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 KWPWWPWRRKHEAEPEAEPIMILKKWPWWPWRRK 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                          taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RWPWWPWRRK - - -
                                                                                                                                                                                                                                      JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page
  can provide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fungus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28 AA;
                                                                                                                                                                                                                                       McNicol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15;
                                                                                                                                                                                                                                                                                           98US-0030619.
97US-0040649.
97US-0915314.
97US-0060099.
                                                                                                                                                                                                                                                                                                                                                                98WO-CA00190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      parasite; virus
                                                                                                                                                                                                                                                                  BIOTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peptide;
                                                                                                                                                                                                                                       PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58.7%;
58.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; resistance; cationic peptide; antibiotic;
tolerance; antibacterial; microorganism;
  synergistic activity against a microorganism that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MBI 11B20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ·---ILMRWPWWPWRRK
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                                                                                                                                                                                                                                       West MHP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 141.5;
Pred. No. 3.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11;
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RESULT 3
AAY44668
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          is tolerant, inherently resistant, antibiotic agent. They can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Crosslinked indolicidin analog; X-indolicidin; poly-Indol 1-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY44668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY44668 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                parasites and viruses.
                                                                                                                                                                                                                                                                               Cleavage-site
                                                                                                                                                                                                                                                                                                    Cleavage-site
                                                                                                                                                                                                                                                                                                                       Cleavage-site
                                                                                                                                                                                                                                                                                                                                            Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                           Key
                                                                                                                                                                                                                                                                                                                                                                                                                                               HIV-1; gram positive bacteria; gram negative; Staphylococcus aure
Escherichia coli; Salmonella typhimurium; yeast; fungi; protozoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   stability; bovine neutrophil; anti
protozoacide; virucide; anti-HIV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Poly-(Indol (1-13)-Met-Ala-Arg-Ile-Ala-Met)3 protein.
                                                                                                                                                                                                                    Cleavage-site
                                                                                                                                                                                                                                        Cleavage-site
                                                                                                                                                                                                                                                             Cleavage-site
                                                                                                                                                                                                                                                                                                                                                               Region
                                                                                                                                                                                                                                                                                                                                                                                              Hos sp.
                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                            hexapeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                       Candida albicans;
WPI; 2000-147133/13
                     Selsted ME,
                                      (REGC ) UNIV
                                                            18-JUN-1998;
                                                                                                                        WO9965510-A1
                                                                                                                                                      Region
                                                                                                                                                                           Region
                                                                                                                                                                                               Region
                                                                                 20-MAY-1999;
                                                                                                     23-DEC-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KWPWWPWRRKHEAEPEAEPIMILKKWPWWPWRRK 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            spacer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                   Osapay K;
                                         CALIFORNIA
                                                            9805-0099631
                                                                                 99WO-US11165
                                                                                                                                                                                                                     /label=
58..59
                                                                                                                                                       /label=
58..63
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39..40
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25..26
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39..44
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                                                                                                                                                                                                /label=
20..25
                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                  /label=
                                                                                                                                                                                                                                                                                                                                                       /label=
                                                                                                                                                                                                                                                  /label=
                                                                                                                                                                                                                                                                                                             /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                      Cryptococcus neoformans; Giardia; Acanthamoeba;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57.1%;
61.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           can be used
                                                                                                                                                                                                                                Cyanogen_bromide_cleavage_site
                                                                                                                                                                                                                                                  Cyanogen_bromide_cleavage_site
                                                                                                                                                                                                                                                                       Cyanogen_bromide_cleavage_site
                                                                                                                                                                                                                                                                                          Cyanogen_bromide_cleavage_site
                                                                                                                                                                                                                                                                                                                                   Enterokinase_cleavage_site
                                                                                                                                                                                                          Cyanogen_bromide_cleavage_site
                                                                                                                                                                                                                                                                                                               Cyanogen_bromide_cleavage_site
                                                                                                                                                                                                                                                                                                                                                      Enterokinase_recognition_site
                                                                                                                                            Hexapeptide_spacer
                                                                                                                                                                 Hexapeptide_spacer
                                                                                                                                                                                     Hexapeptide_spacer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 137.5; DB 1
Pred. No. 1.1e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antimicrobial; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         IV; human immunodeficiency virus-1;
gram negative; Staphylococcus aureus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or has acquired resistance for killing e.g. bacteria,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fungicide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fungi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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RESULT 4
AAY57142
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                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                Matches
               Disclosure; Fig 6; 62pp; English
                             WPI; 2000-053028/04.
N-PSDB; AAZ45123.
                                                                                                                                                                     Synthetic
                                                                                                                                                                                         Indolicidin analogue; antimicrobial activity; helminth; bacteria;
treatment; inhibit growth; micro-organism; contact lens solution;
                                                                                                                                                                                                                                                             AAY57142 standard;
                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Crosslinked indolicidin analogs with antimicrobial activity against bacteria, yeast, fungi, protozoa and viruses \,
                                                                            Selsted ME;
                                                                                                          12-MAY-1998;
                                                                                                                         05-MAY-1999;
                                                                                                                                        18-NOV-1999
                                                                                                                                                      WO9958141-A1
                                                                                                                                                                                    transgenic
                                                                                                                                                                                                                Indolicidin
                                                                                                                                                                                                                                28-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAZ49764
                                                                                          (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                   11
                                                                                                                                                                                                                                                                                                                4 KWPWWPWRRKHEAEPEAEPIMILK-KWPWWPWRR 36
                                                                                                                                                                                                                                                                                                  KWPWWPWRRM-----ARIAMILPWKWPWWPWRR 38
the amino acid sequence of an example of a fusion
                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                           X-indolicidin analog precursors in sufficient quantities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1C; Fig 1; 53pp; English
                                                                                                                                                                                   plant;
                                                                                                                                                                                 inhibit growth; micro-organism;
plant; surgical instrument; yeas
                                                                                                                                                                                                                                                                                                                                                               63 AA;
                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                fusion
                                                                                                                                                                                                                               (first entry)
                                                                                                         98US-0076227
                                                                                                                         99WO-US09942.
                                                                                                                                                                                                                peptide amino
                                                                                                                                                                                                                                                              Protein;
                                                                                                                                                                                                                                                                                                                                      55.4%;
64.7%;
                                                                                                                                                                                                                                                              63
                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                      Score 133.5; DB Pred. No. 9e-10;
                                                                                                                                                                                                                                                              A
                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                acid sequence
                                                                                                                                                                                  yeast; fungi; protozoa
                                                                                                                                                                                                                                                                                                                               5;
                                                                                                                                                                                                                                                                                                                                              21;
                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                              Length
protein which
                                                                                                                                                                                                                                                                                                                                              63;
                                                                                                                                                                                                                                                                                                                               7;
                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                 virus;
                                                                                                                                                                                                                                                                                                                               2
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RESULT 5
AAW12899
Вþ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xaa9 = at least one amino acid;
provided that if Xaa1 is present, Xaa8 = Hse, Met or Met-Xaa9-Met;
and further provided that: if Xaa2 is absent, Xaa1 is absent; if Xaa3 is
absent, Xaa1 and Xaa2 are absent; if Xaa4 is absent, Xaa1, Xaa2 and Xaa3
are absent; and if Xaa5 is absent, Xaa1, Xaa2, Xaa3 and Xaa4 are absent.
The indolicidin analogues can be used to create a fusion polypeptide
consisting of the analogue linked to a peptide. The indolicidin
analogues have antimicrobial activity against gram positive bacteria,
gram negative bacteria, yeast, fungus, protozoa and viruses (e.g. HIV-1).
They are also active against helminths. The analogues can be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   reducing or inhibiting growth or survival of a microorganism. They can be used for treating infections. They can also be included in a liquid such as water or an aqueous solution, e.g. contact lens solution. The analogues have potential uses in food products, and in objects such as the surface of an instrument used to prepare food or to perform surgery. Transgenic plants or animals useful in the food industry can be produced by introducing a nucleic acid molecule encoding an indolicidin analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xaa4 = Xaa5 = Xaa6 = Xaa7 = Xaa8 = Xaa9 = Xa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xaa2 =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   consists of an indolicidin analogue linked to another peptide. Peptides AAY57109 Y57138 and AAY57143-Y57144 are new indolicidin analogues, which have a homoserine residue and/or a truncated amino terminal region. The analogues have the following amino acid sequence:
                       Falla TJ,
                                                                                                                                                                                            23-AUG-1996;
                                                                                                                                                                                                                                                    06-MAR-1997.
                                                                                                                                                                                                                                                                                                             WO9708199-A2
                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                            Shigella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         antiviral;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bacterium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antimicrobial cationic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW12899 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Where:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xaal-Xaa2-Xaa3-Xaa4-Xaa5-Xaa6-Pro-Xaa6-Xaa6-Pro-Xaa6-Xaa7-Xaa7-Xaa8
                                                                             (UYBR-) UNIV BRITISH COLUMBIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 into the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 KWPWWPWRRM-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 KWPWWPWRRKHEAEPEAEPIMILK-KWPWWPWRR 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Trp, Phe or absent;
Arg, Lys or absent;
Trp or Phe;
Arg, Lys or absent;
Arg, Lys or absent;
homoserine (Hse), Met, Met-xaa9-Met or absent, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ile, Leu, Val, Ala, Gly
Ile, Leu, Val, Ala, Gly
Pro or absent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l Similarity
22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              germline cells of such organisms.
                    Gough M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   viral; antitumour; food; preservative; inhibitor; growth;
yeast; endotoxaemia; sepsis; antibiotic; fungal;
Candida albicans; sterilant; Salmonella; Yersina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA;
                                                                                                                                   95US-0002687
                                                                                                                                                                                            96WO-IB00996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55.4%;
                       Hancock REW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -ARIAMILPWKWPWWPWRR 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 133.5;
Pred. No. 9e-1
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or absent; or absent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CP-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .5; DB
9e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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2:

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RESULT 6
AAY24582
ID AAY2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δÃ
DRY PARK TO THE PRINCE OF THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents a specifically claimed novel isolated CC cationic peptide which has antimicrobial activity. The amino acid CC sequence of antimicrobial cationic peptides (including the present CC sequence) is selected from: XIXIPTOXXXXXPTO(XXXPTO)XXX3(X5)0; CC XIXIPTOXXXX4(X5)PTOXXXXXX; XIXIPTOXXXXXPTO(XXXPTO)XXX3(X5)0; CC XIXIXXXXXPTO(XXXPTO)XX2(X5)M; where m = 1-5; n = 1-2; o = 2-5; r CC = 0-8; u = 0-1; X1 = Ile, Leu, Val, phe, Tyr, Typ or Met; X2 = Typ or CC Pro. The peptides are preferably amidated or carboxymethylated. The CC peptides may be used in methods for inhibiting the growth of a bacterium CC or yeast, or for inhibiting an endotoxaemia or sepsis associated CC disorder in a subject. The peptides have a broad activity against the CC medically important fungus Candida albicans. In addition, the peptides are useful as antitumour agents and/or antiviral agents. The peptides CC may be used as sterilants or preservatives of materials susceptible to CC microbial or viral contamination, e.g. in processed foods to inhibit CC salmonella, Yersina and Shigella. The peptides are compact and tend to CC possess the ability to work synergistically with antibitics, and in cardition activity against the possess the ability to work synergistically with antibitics, and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cationic peptide(s) having anti-microbial activity - used for the inhibition of bacterial and viral growth, as an antitumour agent,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1997-179179/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY24582 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
WPI; 1998-169090/15
                                                                                                                                                                               13-JAN-1997;
21-AUG-1996;
                                                         Erfle D,
                                                                                                                (MICR-) MICROLOGIX BIOTECH INC
                                                                                                                                                                                                                                                                    21-AUG-1997;
                                                                                                                                                                                                                                                                                                                           26-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                additive; shampoo; soap;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antimicrobial; antibiotic; antiarrythmic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indolicidin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indolicidin analogue #34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ۳
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ILKKWPWWPWRRKHEAEPEAEPIMILKKWPWWPWRRK 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         as a food preservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     technical material
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l Similarity
16; Conserv
                                                            Fraser JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  some of then possess anti-endotoxin activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bacterial infection; photo-oxidised solubiliser;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA;
                                                                                                                                                                               97US-0034949.
96US-0024754.
                                                                                                                                                                                                                                                                 97WO-US14779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41.3%;
                                                         Krieger TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   insecticide; herbicide; preservative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 99.5; Di
Pred. No. 3.7e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -WPWWPWRRK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99.5;
No. 3
                                                         Taylor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .7e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           surface disinfectant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 18;
                                                            'n
                                                               West
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                               MH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16;
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RESULT 7
AAY91806
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Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aureus, Listeria, Clostridium, rotavirus and papilloma virus. Compounds derived from the analogues may be used similarly; the compounds may also be prepared from antibiotics or antiarrythmic agents. The analogues may be used therapeutically or to coat medical devices; also they are useful as surface disinfectants, as additives to shampoo or soaps, as insecticides or herbicides, or as preservatives for foods and technical materials. The analogues are administered by injection, lavage, orally or topically, generally at 0.1-50 mg/kg. These analogues have a broader spectrum of activity than indolicidin and modification as compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      where Z = P or V; X = hydrophobic residue, preferably W; B = basic aa, preferably R or K; AA = any aa; n = 0 or I; in (II), at least 1 Z = V; in (VIII) at least 2 X = F or Y. The analogues are used to treat infections caused by bacteria (Gram positive or negative, or anaerobic); fungi (yeast or moulds); parasites (protozoa, nematodes, cestodes or trematodes) or viruses. Typical of very many pathogens that can be controlled are Leishmania, Trypanosoma, Ascaris lumbricoides, Fasciola hepatica, Klebsiella pneumoniae, Bordetella pertussis, Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (I)-(VIII)
(II), BBBX2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 13; Page 89; 129pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid - vectors, transformed cells and antibodies, also conjugates with polyoxyalkylene glycol and fatty acid to reduce toxicity, useful therapeutically, as disinfectants etc.
                                                                                                                                                                                                                                                                      Cationic peptide; tumour; pharmaceutical composition; cancer; treatment; leukaemia; polyoxyalkylene-modified; APO; lymphoma; multiple myeloma; breast; lung; ovary; cervix; uterus; skin; prostate; liver; colon; multidrug resistance.
                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                        06-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                          AAY91806;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY91806 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY24549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New indolicidin analogues with antimicrobial activity and related
                                                                                                                                                14-JUN-1999;
                                                                                                                                                                                                              W09965506-A2
                                                                                                                                                                                                                                                                                                                                                         Amino acid sequence of cationic peptide MBI 11D4CN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 reduces their toxicity.
                                                                              (MICR-) MICROLOGIX BIOTECH INC
                                                                                                                                                                               23-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ш
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ILKKWPWWPWRRKHEAEPEAEPIMILKK 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LBBnXZnXXZnXRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ILKKWPWWPWRRK------MILKK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BBBXZXXZXB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
                                                                                                                98US-0096541.
                                                                                                                                                99WO-CA00552
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41.1%;
64.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 99;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .9e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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1;

WPI; 2000-223549/19 Friedland HD,

Krieger TJ,

Taylor

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Erfle

D,

Fraser

JR,

West MHP;

Q 밁

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RESULT 8
AAY24571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents a cationic peptide amino acid sequence, which can be used in the pharmaceutical composition of the invention. The invention relates to a pharmaceutical composition containing at least one activated polyoxyalkylene (APO)-modified cationic peptide. The modification of peptides with APO increases their activity against tumour cells, including those with a multidrug resistant phenotype. The pharmaceutical composition can be used to treat tumours, specifically lymphoma, leukaemia, multiple myeloma, or tumours of breast, lung, ovary, cervix, uterus, skin, prostate, liver and colon.
ANY24549 to ANY24615 represent indolicidin analogues of formula (I)-(VIII) containing up to 25 amino acids (aa): RXZXXZKB (I), (II), BBBXXXXXZKB (III), BZXXXZXBBBHQ(AA)NMILBBAGS (IV), BZXXXXZBBBHQ(V), LBBNXZNXZNRKK (VI), LKNXZXXZRRK (VII) and BBXZXXZXBBH (V), LBBNXZNXZNRKK (VI) and BBXZXXZXBBH (V), LBBNXZNXZNRKK (VI) and BRXZXXZXBBH (V), LBBNXZNXZNRK (VII) and BRXZXXZXBBH (VII) and LBNXZXXZXBH (VII) and LBNXZXXZXBH (VIII) at least 2 X = F or Y. The analogues are used to treat in (VIII) at least 2 X = F or Y. The analogues are used to treat
                                                                                                                                  Claim
                                                                                                                                                          New indolicidin analogues with antimicrobial activity and nucleic acid - vectors, transformed cells and antibodies, conjugates with polyoxyalkylene glycol and fatty acid to toxicity, useful therapeutically, as disinfectants etc.
                                                                                                                                                                                                                                                                                                                                             13-JAN-1997;
21-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel pharmaceutical composition containing optionally activated polyoxyalkylene-modified cationic peptides, useful for treating tumours
                                                                                                                                                                                                                                                                                                                                                                                               21-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                 26-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9807745-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               additive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antimicrobial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY24571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY24571 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 15;
                                                                                                                                                                                                                                                                                                               (MICR-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              food;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indolicidin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indolicidin analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1998-169090/15
                                                                                                                                  12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               technical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18;
                                                                                                                                                                                                                                                                                                               MICROLOGIX BIOTECH INC.
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18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               shampoo;
                                                                                                                               Page 89; 129pp;
                                                                                                                                                                                                                                                                               Fraser JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bacterial infection; photo-oxidised solubiliser;
1; antibiotic; antiarrythmic; surface disinfectant;
ampoo; soap; insecticide; herbicide; preservative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                             97US-0034949.
96US-0024754.
                                                                                                                                                                                                                                                                                                                                                                                             97WO-US14779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94pp;
                                                                                                                                                                                                                                                                               Krieger
                                                                                                                               English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 99;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred.
                                                                                                                                                                                                                                                                               ΤJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A
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                                                                                                                                                                                                                                                                             Taylor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .9e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21;
                                                                                                                                                                                                             activity and
                                                                                                                                                                                                                                                                               West
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21;
                                                             XB (I), BXZXXZXB
BXZXXZXBB(AA)nM
                                                                                              formulae
                                                                                                                                                                              reduce
                                                                                                                                                                                                             related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10;
               basic aa, t 1 Z = V;
                                               (VIII).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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fungi (yeast or moulds); parasites (protozoa, nematodes, cestodes or trematodes) or viruses. Typical of very many pathogens that can be controlled are Leishmania, Trypanosoma, Ascaris lumbricoides, Fasciola hepatica, Klebsiella pneumoniae, Bordetella pertussis, Staphylococcus aureus, Listeria, Clostridium, rotavirus and papilloma virus. Compounds derived from the analogues may be used similarly; the compounds may also be prepared from antibiotics or antiarrythmic agents. The analogues may be used therapeutically or to coat medical devices; also they are useful as surface disinfectants, as additives to shampoo or soaps, as insecticides or herbicides, or as preservatives for foods and technical materials. The analogues are administered by injection, lavage, orally or topically, generally at 0.1-50 mg/kg. These analogues have a broader spectrum of activity than indolicidin and modification as compounds
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               infections caused by bacteria (Gram positive or negative,
                                                                                                            their
AA;
                                                                                                       toxicity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     anaerobic);
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Q
Ър
                             Matches
                                           Query Match
                                     Local
1 ILKKWPWWPWRRKHEAEPEAEPIMILKK
                             18;
                                     Similarity
                             Conservative
                                    40.7%;
64.3%;
IMILKK
                             0;
                                    Score 98; I
Pred. No. 7.
                             Mismatches
              28
                                           DΒ
                                    ,8e-06;
                             0
                             Indels
                             10;
                            Gaps
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1;

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RESULT 9
AAY91808
Amino acid sequence of cationic
                                               AAY91808;
                                                                    AAY91808
                                                                    standard;
                      (first entry)
                                                                    Peptide;
                                                                    21
                                                                    A
 peptide MBI 11D6CN
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leukaemia; po breast; lung; Cationic peptide; tumour; pharmaceutical composition; cancer; treatment; polyoxyalkylene-modified; ng; ovary; cervix; uterus; APO; skin; lymphoma; multiple myeloma;
prostate; liver; colon; prostate;

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Synthetic
                     multidrug resistance
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(MICR-) MICROLOGIX BIOTECH 12-JUN-1998; 14-JUN-1999; 98US-0096541 99WO-CA00552 INC.

WPI; 2000-223549/19 HD Krieger ТJ, Taylor R, Erfle Ď Fraser JR, West MHP;

Disclosure; Page 15; 94pp; English.

polyoxyalkylene-modified Novel pharmaceutical composition

cationic

containing c peptides,

optionally useful for

treating tumours activated

This sequence represents a cationic peptide amino acid sequence, which can be used in the pharmaceutical composition of the invention. The invention relates to a pharmaceutical composition containing at least one activated polyoxyalkylene (APO)-modified cationic peptide. The modification of peptides with APO increases their activity against tumour cells, including those with a multidrug resistant phenotype. The pharmaceutical composition can be used to treat tumours, specifically lymphoma, leukaemia, multiple myeloma, or tumours of breast, lung, ovary, carries and the contains the co uterus,

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RESULT 10
AAY24570
Qγ
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                                           Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY24570 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indolicidin; bacterial infection; photo-oxidised solubiliser;
antimicrobial; antibiotic; antiarrythmic; surface disinfectant;
additive; shampoo; soap; insecticide; herbicide; preservative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-AUG-1999
                                                                                                                                                                                                                                 New indolicidin analogues with antimicrobial activity and related nucleic acid - vectors, transformed cells and antibodies, also conjugates with polyoxyalkylene glycol and fatty acid to reduce toxicity, useful therapeutically, as disinfectants etc.
                                                                                                                                                                                                                                                                                                                                                                                                       WO9807745-A2
                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indolicidin
         insecticides or herbicides, or as preservatives for foods and technical materials. The analogues are administered by injection, lavage, orally or topically, generally at 0.1-50 mg/kg. These analogues have a broader spectrum of activity than indolicidin and modification as compounds
                                                                                                                                                                                                                Claim 12; Page 89; 129pp; English.
                                                                                                                                                                                                                                                                                 WPI; 1998-169090/15.
                                                                                                                                                                                                                                                                                                                     (MICR-) MICROLOGIX BIOTECH INC.
                                                                                                                                                                                                                                                                                                                                        21-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                13-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                  21-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                    26-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ILKKWPWWPWRR-----IMILKK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ILKKWPWWPWRKHEAEPEAEPIMILKK 28
                                                                                                                                                                                                                                                                                                                                                                                                                                         ive; shampoo; soap;
technical material.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l Similarity
18; Conserv
                                                                                                                                                                                                                                                                                                   Fraser JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      analogue #22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA;
  toxicity
                                                                                                                                                                                                                                                                                                                                       97US-0034949.
96US-0024754.
                                                                                                                                                                                                                                                                                                                                                                   97WO-US14779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40.7%;
64.3%;
                                                                                                                                                                                                                                                                                                   Krieger TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 98; I
Pred. No. 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ΑA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                     Taylor R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 21;
7.8e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                     West MH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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RESULT 11
AAY91807
ID AAY91
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                                                                                             PYX
Qq
B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 17; Conser
                                               Matches
                                                        Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                        This sequence represents a cationic peptide amino acid sequence, which can be used in the pharmaceutical composition of the invention. The invention relates to a pharmaceutical composition containing at least one activated polyoxyalkylene (APO) modified actionic peptide. The modification of peptides with APO increases their activity against tumour cells, including those with a multidrug resistant phenotype. The pharmaceutical composition can be used to treat tumours, specifically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cationic peptide; tumour; pharmaceutical composition; cancer; treatment; leukaemia; polyoxyalkylene-modified; APO; lymphoma; multiple myeloma; breast; lung; ovary; cervix; uterus; skin; prostate; liver; colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY91807 standard; Peptide; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9965506-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      multidrug resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY91807;
                                                                                                                lymphoma, leukaemia, multiple myeloma, or cervix, uterus, skin, prostate, liver and
                                                                                                                                                                                                                                                                        Novel pharmaceutical composition containing polyoxyalkylene-modified cationic peptides,
                                                                                                                                                                                                                                                                                                                                                                                                            14-JUN-1999;
                                                                                             Sequence
                                                                                                                                                                                                                                       Disclosure; Page 15; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                     12-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                           (MICR-) MICROLOGIX BIOTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ILKKWPWWPWRKHEAEPEAEPIMILKK 28
μ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ILKKWPWWPWRR------MILKK 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ILKKWPWWPWRRKHEAEPEAEPIMILKK 28
                                                                                                                                                                                                                                                                                                              2000-223549/19.
                                              l Similarity
17; Conserv
                                                                                                                                                                                                                                                                                                                                      HD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence of cationic peptide MBI 11D5CN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20
                                                                                              20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA;
                                                                                                                                                                                                                                                                                                                                     Krieger TJ,
                                                                                                                                                                                                                                                                                                                                                                                     98US-0096541
                                                                                                                                                                                                                                                                                                                                                                                                            99WO-CA00552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38.8%;
                                                           38.8%;
60.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                       Taylor R,
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  MILKK 17
                                               0;
                                                           Score 93.5;
Pred. No. 2
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                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                       Erfle D,
                                                             .7e-05;
                                                                                                                      tumours of colon.
                                                                         DB
                                                                                                                                                                                                                                                                             poptionally useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19;
                                                                         21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                   0
                                                                                                                                                                                                                                                                                                                                        Fraser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                    of breast,
                                                                         Length
                                                                                                                                                                                                                                                                            activated treating tumours
                                                                                                                                                                                                                                                                                                                                          JR,
                                                                          20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11;
                                                   11;
                                                                                                                                                                                                                                                                                                                                          West MHP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                   1;
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RESULT 12 AAW12873 ID AAW12

AAW12873 standard; peptide;

13

A

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RESULT 13
AAY24609
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                                                                                               밁
                                                               Query Match
Best Local S
Matches 13
                                                                                                            N.B. The present sequence represents SEQ ID NO:1 in the claims and examples of the specification, but differs slightly from the SEQ I in the sequence listing on page 51 of the specification (see AAW27 \,
                                                                                                                                                                                                                                                                                                  The present sequence represents a specifically claimed novel cationic peptide which has antimicrobial activity. The amino
                                                                                                                                                                                                                                                                                                                                           Cationic peptide(s) having anti-microbial activity - used for the inhibition of bacterial and viral growth, as an antitumour agent, and as a food preservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacterial; viral; antitumour; food; preservative; inhibitor; bacterium; yeast; endotoxaemia; sepsis; antibiotic; fungal; antiviral; Candida albicans; sterilant; Salmonella; Yersina;
                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                             Claim
                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-179179/16
                                                                                                                                                                                                                                                                                                                                                                                            Falla
                                                                                                                                                                                                                                                                                                                                                                                                                           23-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                           23-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W09708199-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shigella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antimicrobial cationic peptide CP-11
                                                                                                                                                                                                                                                                                                                                                                                                           (UYBR-) UNIV BRITISH COLUMBIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-DEC-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW12873;
                                _
                                               \vdash
                              ILKKWPWWPWRRK 13
                                                                                                                                                                                                                                                                                                                           2; Page 65; 89pp; English.
                                                                       Similarity
                                                                                               13
                                                                                                                                                                                                                                                                                                                                                                                          Gough M,
                                                              Conservative
                                                                                               A
                                                                                                                                                                                                                                                                                                                                                                                                                           95US-0002687
                                                                                                                                                                                                                                                                                                                                                                                                                                          96WO-IB00996
                                                                                                                                                                                                                                                                                                                                                                                           Hancock REW;
                                                               0
                                                                      Score 91;
Pred. No.
                                                              Mismatches
                                                                      DB 18;
3.5e-05;
                                                                             Length 13
                                                              Indels
                                                              0,
                                                                                                             AAW27179).
                                                                                                                                                                                                                                                                                                           isolated
                                                              Gaps
                                                                                                                     ID NO:1
                                                              0;
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RESULT 14 AAW66378

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1 ILKKWPWWPWRRK 1 ILKKWPWWPWRRK

δÃ

Gaps

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C(V), LBBNZNXZNXRK (VII), PAZAAABBBH (VII) and BNZXXZXXBBB (VIII).

C(W), LBBNZNXZNXRK (VII), LRANZXXZRRK (VII) and BNZXXZXBBB (VIII).

C(Preferably R or K; AA = any aa; n = 0 or 1; in (II), at least 1 Z = V; in (VIII) at least 2 X = F or Y. The analogues are used to treat infections caused by bacteria (Gram positive or negative, or anaerobic); in (VIII) at least 2 X = F or Y. The analogues are used to treat infections caused by bacteria (Gram positive or negative, or anaerobic); in (VIII) at least 2 X = F or Y. The analogues are used to treat infections caused by bacteria (Gram positive or negative, or anaerobic); in (VIII) at least 2 X = F or Y. The analogues are used to treat infections or viruses. Typical of very many pathogens that can be controlled are Leishmania, Trypanosoma, Ascaris lumbricoides, Fasciola in Partica, Klebsiella pneumoniae, Bordetella pertussis, Staphylococcus in Controlled are Leishmania, Trypanosoma, Ascaris lumbricoides, Fasciola in Partico, Klebsiella pneumoniae, Bordetella pertussis, Staphylococcus in Controlled are Leishmania, Trypanosoma, Ascaris lumbricoides, Fasciola in Partico, Klebsiella pneumoniae, Bordetella pertussis, Staphylococcus in Controlled are Leishmania, Trypanosoma, Ascaris lumbricoides, Fasciola in Particolled from the analogues may be used similarly; the compounds may in the prepared from antibiotics or antitarrythmic agents. The analogues in a controlled in the prepared from antibiotics or antitarrythmic agents. The analogues in the prepared from antibiotics or antitarrythmic agents. The analogues are administered by injection, lavage, orally or topically, generally at 0.1-50 mg/kg. These analogues have a broader in the interval and modification as compounds in the interval and modification 
          Matches
                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY24549 to AAY24615 represent indolicidin analogues of formulae (I)-(VIII) containing up to 25 amino acids (aa): RXZXXZXB (I), BXZXXZXB (II), BBSXXXXZXB (III), BBSXXXXZXB (III), BBSXXXXZXB (III), BBSXXXXZXB (III), LKDXZXXZXBRK (VII) and BBXZXXZXBBB (VIII).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New indolicidin analogues with antimicrobial activity and related nucleic acid - vectors, transformed cells and antibodies, also conjugates with polyoxyalkylene glycol and fatty acid to reduce toxicity, useful therapeutically, as disinfectants etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indolicidin; bacterial infection; photo-oxidised solubiliser; antimicrobial; antibiotic; antiarrythmic; surface disinfectant; additive; shampoo; soap; insecticide; herbicide; preservative; food; technical material.
                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-169090/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Erfle D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-JAN-1997;
21-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 32; 129pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9807745-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY24609 standard; peptide; 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MICR-) MICROLOGIX BIOTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indolicidin analogue #61.
                              Similarity
                                                                                                                                                   their toxicity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fraser JR,
                                                                                                       13
          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                     ΑA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97US-0034949
96US-0024754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97WO-US14779
                              100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Krieger TJ,
          0
                              Score 91;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A
          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Taylor
DB 1>,
J. 3.5e-05;
O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ₩,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      West
                                                     Length 13
       Indels
     0;
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AAW71690
ID AAW7
XX
AC AAW7
AC AAW7
DT 11-J
XX
DE Cati
XX
KW MBI1
KW repl
                                                                                                                                                                                                                           Дb
                                                                                                                                                                                                                                                      Qy
                                                                                                                                                                               RESULT 15
                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-FEB-1998;
10-MAR-1997;
20-AUG-1997;
26-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents a specifically claimed cationic peptide from the present invention. The present invention describes compositions and methods for treating infection, especially bacterial infections. The compositions and methods use cationic peptides in combination with an antibiotic agent which are then administered to a patient to enhance the activity of the antibiotic agent, to overcome: (a) tolerance; (b) activity of the antibiotic agent, to overcome: (b) tolerance; (c) inherent resistance. The combinations of antibiotics and cationic peptides can provide synergistic activity against a microorganism that is tolerant, inherently resistant, or has acquired resistance to an antibiotic agent. They can be used for killing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cationic peptide of claim 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW66378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New indolicidin peptide analogues - useful for, e.g. enhancing activity of antibiotic or overcoming tolerance, acquired resistance or inherent resistance of microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9840401-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bacteria; fungus; parasite; virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indolicidin analogue; resistance; cationic peptide; antibiotic;
bacterial infection; tolerance; antibacterial; microorganism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW66378 standard; peptide; 13 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-520800/44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fraser JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MICR-) MICROLOGIX BIOTECH INC.
              MBI11; cationic peptide; plasmid pKL1; small cryptic plasmid;
replication; RepA; vector; RAMP.
                                                                                                                                                                                                                                                                                                                                               Sequence
                                                          Cationic peptide MBI11 (MW 1879).
                                                                                                                                                 AAW71690 standard; Peptide; 13 AA
                                                                                         11-JAN-1999
                                                                                                                     AAW71690;
                                                                                                                                                                                                                                                                                                                                                                          .g. bacteria, fungi, parasites and viruses.
                                                                                                                                                                                                                           1 ILKKWPWWPWRRK 13
                                                                                                                                                                                                                                                         1 ILKKWPWWPWRRK 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 93; 105pp; English
                                                                                                                                                                                                                                                                                                                                                 13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              McNicol
                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0030619.
97US-0040649.
97US-0915314.
97US-0060099.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98WO-CA00190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . рJ,
                                                                                                                                                                                                                                                                                       37.8%; Score 91; DB 19; 1
100.0%; Pred. No. 3.5e-05;
Nismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                West MHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #5
                                                                                                                                                                                                                                                                                                                   Length 13;
                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                            0;
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Search completed: January 15, 2003, 18:08:34 Job time : 36 secs

0;

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QУ
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                                                                   Query Match
Best Local S
                                                        Matches
                                                                                                                                           MBIII is a small (mol.wt. 1879) cationic peptide. DNA encoding MBIII has been incorporated into vector px2h-Bl, in which the replication leader (R2l) sequence of RepA (see also AAW71686) is joined to 2 Hpro peptides (see also AAW71692), to provide a vector for expression of MBIII in host cells. The invention provides controlled replication plasmid vectors (RAMP vectors) comprising a replication origin of a small cryptic plasmid and a gene encoding RepA. The vectors can reach very high levels of plasmid replication, but are not lethal to the host cell, and can be used to direct the high level expression of e.g. cytokines, antigens and therapeutic proteins.
                                                                                                                                                                                                                                                                                                                                                         Increasing plasmid copy number in a cell with the repA gene product - and an small cryptic plasmid ori sequence, useful for high level expression of e.g. cytokines, antigens or therapeutic proteins % \left( 1\right) =\left( 1\right) ^{2}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-531571/45
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Burian J, Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9841636-A2
                                                                                                                                                                                                                                                                                                                                  Example 13; Page 54; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BURI/) BURIAN J.
(KAYW/) KAY W W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-MAR-1997;
                                                                                                                   Sequence
1 ILKKWPWWPWRRK 13
              1 ILKKWPWWPWRRK 13
                                                  ch 37.8%;
l Similarity 100.0%;
l3; Conservative (
                                                                                                                      13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97US-0040722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98WO-CA00214.
                                                            Score 91; DB
;; Pred. No. 3.5
0; Mismatches
                                                          0;
                                                                          DB 19;
3.5e-05;
                                                                                        Length 13;
                                                               Indels
                                                                                                                                                                                    and can
                                                               0
                                                               Gaps
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OM protein - protein search, using sw model
                                                                                       GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
```

Run on: December 11, 2002, 15:37:24; Search time 28 Seconds (without alignments) 272.277 Million cell updates/sec

Title: Perfect score:

Scoring table: Sequence: US-09-444-281-35-27-35 241 1 ILKKWPWWPWRRKHEAEPEAEPIMILKKWPWWPWRRK 37

Searched: BLOSUM62 Gapop 10.0 , Gapext 0.5 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database SPTREMBL\_21:\*
1: sp\_archea:\*
2: sp\_bacteria:
3: sp\_fungi:\*
4: sp\_humani:\*
5: sp\_inverteb:
6: sp\_manmal:\*
7: sp\_mhc:\*
8: sp\_organel1:
9: sp\_phage:\* sp\_archea:\*
sp\_bacteria:\*
sp\_fungi:\* sp\_mammal:\*
sp\_mhc:\* sp\_organelle:\* sp\_invertebrate:\*

sp\_vertebrate:\*
sp\_unclassified:\*
sp\_rvirus:\*
sp\_bacteriap:\*
sp\_archeap:\* sp\_rodent:\*
sp\_virus:\*

sp\_plant:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

16	15	14	13	12	11	10	9	œ	7	6	, UI	4	ω	2	1	Result No.
60	61	61	61	61	61	61	62	63	63	63	63	64	67	67.5	70.5	Score
24.9	25.3	25.3	25.3	25.3	25.3	25.3	25.7	26.1	26.1	26.1	26.1	26.6	27.8	28.0	29.3	Query Match
147	985	735	734	284	250	92	367	750	748	192	49	175	723	746	1245	Query Match Length DB
11	15	12	12	10	17	12	11	12	12	16	12	12	12	12	ω	DB S
Q61427	Q98414	Q9DUC9	Q8 <b>V7</b> I1	Q94CI8	Q8TWG0	Q8V7E2	Q63778	Q91D04	Q9DT81	Q928B7	Q9DT80	Q91RD8	Q9DUC4	Q9JH31	Q9Y7V5	ID
					•										•	
Q61427 mus musculu	Q98414 ovine lenti	Q9duc9 tt virus. o	Q8v7il tt virus. o	Q94ci8 lycopersico	Q8twg0 methanopyru	Q8v7e2 tt virus. o	Q63778 rattus norv	Q91d04 tt virus. o	Q9dt81 tt virus. o	Q9z8b7 chlamydia p	0 tt	Q91rd8 tt virus. o	Q9duc4 tt virus. o	Q9jh31 tt virus. o	29y7v5 trichoderma	Description

5	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
56	56	56.5	56.5	56.5	57	57	57	57	57.5	57.5	57.5	57.5	57.5	58	58	58	58	58	58.5	58.5	59	59	59	59.5	59.5	60.	60	60
23.2	23.2	23.4	23.4	23.4	23.7	23.7			23.9		•				24.1	24.1			24.3									
252	252	532	162	157	971	970	426	252	772	444	376	341	117	1300	879	646	513	107	1567	521	739	485	95	2292	114	766	381	242
15	15	16	Ģ	σı	11	11	12	15					15	11	11	11	11	16	N	10	12	16	10	12	16	12	16	17
Q9ITV2	Q9ITX8	Q9CK19	Q9W1W7	Q9Y0E8	070458	088821	Q99AQ7	Q9IU37	Q9BXY6	Q9HC40	094516	Q90644	Q9YRR9	P97692	Q8VI99	Q63779	Q63289	Q9XAE4	Q9ADM1	Q94EF3	Q99AQ3	P72844	Q9LQN0	Q66765	Q9x8C2	Q91CY5	Q9A7E1	8WAI8
human			Q9w1w7 drosophila	Q9y0e8 drosophila	O70458 mus musculu	O88821 mus musculu		Q9iu37 human immun	Q9bxy6 homo sapien	Q9hc40 homo sapien		_	Q9yrr9 human immun	rattus	rattus	rattus						P72844 synechocyst			Q9x8c2 streptomyce		•	Q8tvm8 methanopyru

## ALIGNMENTS

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ACC PROPERTY OF SECONDARY OF SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
Q9DUC4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
Q9JH31
    Query Match
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Best Local Similarity 33.3
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9DUC4
Q9DUC4;
Q1-MAR-2001
01-MAR-2001
01-JUN-2002
                                                                                             MEDLINE-20534983; PubMed-11080484;
Okamoto H., Nishizawa T., Tawara A., Peng Y., Takahashi M.,
Kishimoto J., Tanaka T., Miyakawa Y., Mayumi M.;
"Species-specific TT viruses in humans and nonhuman primate phylogenetic relatedness.";
Virology 277:368-378(2000).
EMBL; AB041959; BAB19313.1; -.
InterPro; IPR004263; Serine_carbpept.
InterPro; IPR004219; TTvirus_Unk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORF1.
TT virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9JH31;
01-OCT-2000
01-OCT-2000
01-JUN-2002
                                              SEQUENCE
                                                             Pfam; PF02956; TT_ORF1; 1.
PROSITE; PS00131; CARBOXYPEPT_SER_SER; UNKNOWN_1
                                                                                                                                                                                                                                                                                           STRAIN-MF-TTV9;
                                                                                                                                                                                                                                                                                                                                                    Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tizuka H., Miyakawa Y., Mayumi M.;
"The entire nucleotide sequences of two distinct isolates (TJN01 and TJN02) remotely related to isolates.";
                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                           Okamoto H
                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-MF-TTV9;
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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EMBL; AB028669; BAA94878.1; ".
InterPro; IPR004219; TTVINS_UNk.
Pfam; PF02956; TT_ORF1; 1.
SEQUENCE 746 AA; 88561 MW; E01
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Viruses; ssDNA viruses; NCBI_TaxID=68887;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=TJN02;
MEDLINE=20456801; PubMed=11003468;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Okamoto
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33.3%;
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Pred. No. 3.2;
2; Mismatches
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01-MAR-2001
01-MAR-2001
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01-DEC-2001
01-DEC-2001
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                                                                                                                                                                                                                                Okamoto H., Nishizawa T., Tawara A., Takahashi M., Sai T., Sugai Y.;
"TT virus mRNAs detected in the bone marrow cells individual.";
                                                                                                                                                                                                                                                                                                                                STRAIN-TYM9
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=68887;
                                                                                                                                                                                                                                                                                                                                                                                                              Viruses;
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                                                                                                                                                                                                                                                                                                                  MEDLINE=20568739;
                                                                                                                                                                                                                                                                                                                                                                                                                                 TT virus.
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  WTWW-WQRRRRR-
                                      WPWWPWRRKHEAEPEAEPIMILKKWPWWPWRRK 37
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10; Conserv
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                                                                               Conservative
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zawa T., Tawara A.,
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16,
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Last annotation updat
                                                                                              Score 63; I
Pred. No. 0
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2; Mismatches
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Pred. No. 2.1;
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Viruses;
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Q9Z8B7;
01-MAY-1999
MEDLINE-20568739; PubMed-11118348;
Okamoto H., Nishizawa T., Tawara A
Sai T., Sugai Y.;
"TT virus mRNAs detected in the bo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K., Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.; "Comparison of whole genome sequences of Chlamydia pneumoniae J138 from Japan and CWL029 from USA."; Nucleic Acids Res. 28:2311-2314(2000). EMBL; AE001625; AAD18570.1; -. EMBL; AE002194; AAF38182.1; -. EMBL; AP002546; BAA98634.1; -. TIGR; CP0327; -.
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CPN0426 OR CPJ0426 OR CP0327.
Chlamydia pneumoniae (Chlamydophila pneumoniae)
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydo
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01-MAR-2001
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Eisen J., Fraser C.M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99206606; PubMed=10192388;
Kalman S., Mitchell W., Marathe R., Lammel C., Fan J.,
Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
"Comparative genomes of Chlamydia pneumoniae and C. tra
                                                                                         STRAIN-TYM9
                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                   NCBI_TaxID=68887;
                                                                                                                                                                                                                                                                                                       Q9DT81;
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K., Bass
Dodson R.
Salzberg
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Best Local
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Q63778; 01-NOV-1996 (TrEMBLrel. 01, Crea
01-NOV-1996 (TrEMBLrel. 17, Last
01-JUN-2001 (TrEMBLrel. 17, Last
Hypothetical 43.7 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORF1.
TT virus.
                                    MEDLINE=87064324; PubMed=3023845; D'Ambrosio E., Waitzkin S.D., Witn "Structure of the highly repeated, or LIRn) of the rat.", Mol. Cell. Biol. 6:411-424(1986).
                                                                                                                             Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                multiple tissues from infect
Virology 288:358-368(2001).
EMBL; AB060592; BAB69900.1;
InterPro; IPR004219; TTvirus
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EMBL; AB050448; BAB1928.1; -.
Interpro; IPR004219; TTYIRUS_Un
Pfam; PF02956; TT_ORF1; 1.
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Yoshikawa A.;
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NCBI_TaxID=68887;
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01-DEC-2001
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          PROSITE;
                  InterPro;
                              EMBL; M13100;
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                                                                                                                   NCBI_TaxID=10116;
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        1. Biol. 6:411-424(1986).
3100; AAA66046.1; -.
; IPR000566; Lipocln_cytFABP.
PS00213; LIPOCALIN; UNKNOWN
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                                                    Witney F.m.
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Sciurognathi;
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humans.";
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01-JUN-2002 (TrEMBLrel. 21, Last sequence of JUN-2002 (TrEMBLrel. 21, Last anno on-JUN-2002 (TrEMBLrel. 21, Last anno on-JUN-2002 (TrEMBLrel. 21, Last anno on-dependent protein deacetylase, S:
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Best Local :
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                    SEQUENCE FROM N.A.

STRAIN=AN19 / DSM 6324 / JCM 9639;

MEDLINE-21927647; PubMed=11930014;

Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N.,

Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,

Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,

Malykh A.G., Koonin E.V., Kozyavkin S.A.;

"The complete genome of hyperthermophile Methanopyrus kandleri AV19

and monophyly of archaeal methanogens.";

Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
     SEQUENCE
               Complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-21844401; Pubmed-11855633;
MEDLINE-21844401; Pubmed-11855633;
MEDLINE-2184401; Pubmed-11855633;
                                                                                                                                          NCBI_TaxID=2320;
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01-MAR-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                    Methanopyrus
                                                                                                                                                             Archaea;
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EMBL; AB064615; BAB79374.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Okamoto
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13; Conserv
                                                                                                                                                           Euryarchaeota;
             proteome
                                                                                                                                                                                                                                                                                                                                                                    92 AA; 12429 MW;
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     ΑĀ;
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     27799 MW;
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20,
21,
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tylase, SIR2 family.
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Pred. No.
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    B051994FE5B24E05 CRC64;
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01-MAR-2002
01-MAR-2002
                                                                      classifiable into the fourth viremic infants.", Arch. Virol. 147:21-41(2002). EMBL; AB064598; BAB79322.1;
                                                                                                                                                                                                                                                                                                              TT virus.
Viruses;
                                                                                                                                                                                                                                                                                                                                           ORF1
                              InterPro; IPR004219; TTvirus_Unk. Pfam; PF02956; TT_ORF1; 1. SEQUENCE 734 AA; 86978 MW; F6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycine-rich protein LeGRP1.
Lycopersicon esculentum (Tomato).
Eukaryota; Viridiplantae; Strepto
                                                                                                                                              Okamoto
                                                                                                                                                       MEDLINE=21844401; PubMed=11855633; Peng Y.H., Nishizawa T., Takahashi M.,
                                                                                                                                                                                      STRAIN=CT43F;
                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                             Submitted (JUL-2001)
                                                                                                                                                                                                                                            Okamoto
                                                                                                                                                                                                                                                         STRAIN=CT43F;
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                            "Analysis of the complete genomes of thirteen TT virus
                                                                                                                                                                                                                                                                                                 NCBI_TaxID=68887;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clycopersicon esculentum).";
Physiol. Plantarum 0:0-0(2001).
EMBL; AY026037: ARAK08984 1: -
SEQUENCE 284 AA; 23434 MW; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "LeGRP1: A new member of glycine-rich
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                             86978 MW; F60E188BC0104A68 CRC64;
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01-FEB-1997
01-DEC-2001
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EMBL; AB041957; BAB19308.1; -. INTELPO; IPR004219; TTVirus_Unk.
Pfam; PF02956; TT_ORF1; 1.
                                                                                                                                                        MEDLINE-95135990; PubMed=7834396; Woodward T.M., Carlson J.O., de la DeMartini J.C.; "Biological and genetic changes in passage in isogeneic twin lambs."; Acquir. Immune Defic. Syndr. Hun
                                                                                                                                                                                                                                                                                                                                                                                                                                             Ovine lentivirus.
Viruses; Retroid viruses;
NCBI_TaxID=11663;
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Carlson J.O., Demartini J.C., Mwaengo D.M.;
"Envelope glycoprotein nucleotide sequence and genetic
                                                                  SEQUENCE FROM N.A.
STRAIN-85/34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9ED818D6BE6FA5D3 CRC64;
                                                                                                                                                                  Hum.
                                                                                                                                                                                               in ovine lentivirus strains following
";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence update)
annotation update)
                                                                                                                                                                                                                                                                                     Concha-Bermejillo
                                                                                                                                                              Retrovirol.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 735;
                                                                                                                                                        8:124-133(1995).
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                                                                                                           Query Match
Best Local
                                                                                               Matches
                                                                                                                                                                      characterization of North American ovine lentiviruses."; Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases. EMBL; U64439; AAB08725.1; -. InterPro; IPR000328; Env_GP41. Pfam; PF00517; GP41; 1.
                                                                                                                                                 SEQUENCE
                                                                                                                                                             Transmembrane
223 VPYPFALLKCTKWCWYP
                                              163 ILKRVYKQDWPWNTYHWPLWQMENMRQWMKENEREYKGRTNKTKEDIDDLLAGKIRGRFC 222
                       22
                                                                                                            Local Similarity
                                                                      1 ILKK-----WPW-----WP----
                       ---PIMILK--KWPWWP 33
                                                                                              18;
                                                                                                                                                985 AA;
                                                                                              Conservative
                                                                                                                                                113794 MW;
                                                                                                           25.3%;
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239
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                                                                      -WRRKHEAEPEAE-
                                                                                                                                                3197258EDBDE3597 CRC64;
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